

Connecting via Winsock to STN

Welcome to STN International! Enter x:x

LOGINID:SSSPTA1636DXS

PASSWORD:

TERMINAL (ENTER 1, 2, 3, OR ?):2

***** Welcome to STN International *****

NEWS 1 Web Page URLs for STN Seminar Schedule - N.
America

NEWS 2 Jan 25 BLAST(R) searching in REGISTRY available in
STN on the Web

NEWS 3 Jan 29 FSTA has been reloaded and moves to weekly
updates

NEWS 4 Feb 01 DKILIT now produced by FIZ Karlsruhe and has a
new update

frequency

NEWS 5 Feb 19 Access via Tymnet and SprintNet Eliminated
Effective 3/31/02

NEWS 6 Mar 08 Gene Names now available in BIOSIS

NEWS 7 Mar 22 TOXLIT no longer available

NEWS 8 Mar 22 TRCTHERMO no longer available

NEWS 9 Mar 28 US Provisional Priorities searched with P in
CA/CAPLUS

and USPATFULL

NEWS 10 Mar 28 LIPINSKI/CALC added for property searching in
REGISTRY

NEWS 11 Apr 02 PAPERCHEM no longer available on STN. Use
PAPERCHEM2 instead.

NEWS 12 Apr 08 "Ask CAS" for self-help around the clock

NEWS 13 Apr 09 BEILSTEIN: Reload and Implementation of a New
Subject Area

NEWS 14 Apr 09 ZDB will be removed from STN

NEWS 15 Apr 19 US Patent Applications available in IFICDB,
IFIPAT, and IFIUDB

NEWS 16 Apr 22 Records from IP.com available in CAPLUS,
HCAPLUS, and ZCAPLUS

NEWS 17 Apr 22 BIOSIS Gene Names now available in
TOXCENTER

NEWS 18 Apr 22 Federal Research in Progress (FEDRIP) now
available

NEWS EXPRESS February 1 CURRENT WINDOWS VERSION IS
V6.0d,

CURRENT MACINTOSH VERSION IS V6.0a(ENG) AND
V6.0Ja(JP),

AND CURRENT DISCOVER FILE IS DATED 05

FEBRUARY 2002

NEWS HOURS STN Operating Hours Plus Help Desk Availability

NEWS INTER General Internet Information

NEWS LOGIN Welcome Banner and News Items

NEWS PHONE Direct Dial and Telecommunication Network Access
to STN

NEWS WWW CAS World Wide Web Site (general information)

Enter NEWS followed by the item number or name to see news on that
specific topic.

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***** STN Columbus *****

FILE 'HOME' ENTERED AT 12:48:41 ON 24 MAY 2002

=> file registry

COST IN U.S. DOLLARS	SINCE FILE	TOTAL
	ENTRY	SESSION
FULL ESTIMATED COST	0.42	0.42

FILE 'REGISTRY' ENTERED AT 12:49:49 ON 24 MAY 2002

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STRUCTURE FILE UPDATES: 22 MAY 2002 HIGHEST RN
420781-77-7

DICTIONARY FILE UPDATES: 22 MAY 2002 HIGHEST RN
420781-77-7

TSCA INFORMATION NOW CURRENT THROUGH July 7, 2001

Please note that search-term pricing does apply when
conducting SmartSELECT searches.

Crossover limits have been increased. See HELP CROSSOVER for
details.

Calculated physical property data is now available. See HELP
PROPERTIES
for more information. See STNote 27, Searching Properties in the CAS
Registry File, for complete details:
<http://www.cas.org/ONLINE/STN/STNOTES/stnotes27.pdf>

=> E "SPOIII/CN 25

E1 1 SPOIID (FUSOBACTERIUM NUCLEATUM
NUCLEATUM STRAIN ATCC25586 GENE FN0806)/CN
E2 1 SPOIID-LIKE DOMAIN CONTAINING PROTEIN;
PEPTIDOGLYCAN-BINDING DOMAIN (CLOSTRIDIUM
ACETOBUTYLICUM STRAIN ATCC 824 GENE CAC2506)/CN
E3 0 --> SPOIII/CN
E4 1 SPOIII-FAMILY MEMBRANE PROTEIN
(MYCOBACTERIUM LEPRAE STRAIN TN GENE ML1541)/CN
E5 1 SPOIII FAMILY PROTEIN (STREPTOCOCCUS
PNEUMONIAE STRAIN TIGR4 GENE SP1975)/CN
E6 1 SPOIII FAMILY PROTEIN (STREPTOCOCCUS
PNEUMONIAE STRAIN TIGR4 GENE SP2041)/CN
E7 1 SPOIII-ASSOCIATED PROTEIN (BACILLUS
HALODURANS STRAIN C-125 GENE JAG)/CN
E8 1 SPOIII-ASSOCIATED PROTEIN (BACILLUS
SUBTILIS GENE JAG)/CN
E9 1 SPOIII-ASSOCIATED PROTEIN (CLOSTRIDIUM
PERFRINGENS STRAIN 13 GENE JAG)/CN
E10 1 SPOIII-ASSOCIATED PROTEIN (JAG) (BORRELIA
BURGDORFERI STRAIN B31 GENE BB0443)/CN
E11 1 SPOIII-ASSOCIATED PROTEIN (JAG)
(TREPONEMA PALLIDUM GENE TP0948)/CN
E12 1 SPOIII-LIKE PROTEIN (STREPTOMYCES
COELICOLOR STRAIN A3(2)/M145 ORF431)/CN
E13 1 SPOIVB PEPTIDASE/CN
E14 1 SPOIVB PROTEINASE/CN
E15 1 SPOIVB SERINE PEPTIDASE/CN
E16 1 SPOLACID/CN
E17 1 SPOLAMID/CN
E18 1 SPOLAMID ZP/CN
E19 1 SPOLAPON AOS/CN
E20 1 SPOLAPREN SN/CN
E21 1 SPOLAPREN X/CN
E22 1 SPOLAPRET/CN
E23 1 SPOLAPRET CS/CN
E24 1 SPOLAPRET OS/CN
E25 1 SPOLARIN/CN

=> S E4

L1 1 "SPOIIIIE-FAMILY MEMBRANE PROTEIN
(MYCOBACTERIUM LEPRAE STRAIN TN GENE ML1541)"/CN

=> DIS L1 1 SQIDE

THE ESTIMATED COST FOR THIS REQUEST IS 5.53 U.S.
DOLLARS

DO YOU WANT TO CONTINUE WITH THIS REQUEST? (Y)/N:Y

L1 ANSWER 1 OF 1 REGISTRY COPYRIGHT 2002 ACS

RN 327136-96-9 REGISTRY

CN SpoIIIIE-family membrane protein (Mycobacterium leprae
strain TN gene

ML1541) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN GenBank AL583922-derived protein GI 13093363

FS PROTEIN SEQUENCE

SQL 1345

SEQ 1 MIGVVVIGLV GGMVAMTFAS GSRVFGGAGS

IFPLFMIGGV AMMMFSGRMG

51 GQQQMSRPKL DAMRAQFMLM LDMLREAANE

SADSM DANYR WFHPAPTTLA

101 AAVGSSRMWE RKPDPGKDLNF CVVRVGVGMT

RPEVTWGE PQ NMPTDIELEP

151 VTGKALQEFGRYQSIYVNLPMVSLVPEPW

YALIGDREQT LGLMRSHICQ

201 LTFSHGPDHV QMVVVSSDLE QWDWVKWLPH

FGDPRRQDAA GNARMVYSSV

251 REFATEQAEL FAGRGSFTR HASSAQTPPT

PHHLIVADV DPEWEYVISV

301 EGIDGVTFDD LTGSSMWTVV PKRTLRFDEK

GVIDALPRDR DTWMVIDDKP

351 WFFALADQLS FAEAEFAQK LAHWRAEAY

EEIGQRVAHI GARDILSYYG

401 IGDPSAIDFD ALWNSRTDAM GKSRLRVPGF

NRSDNGELLF LDMKSLDEGG

451 DPHGVMSGT TGS GKSTLVR TVIESLMLAH

PPEELQFVLA DLKGGSAVKP

501 FAGVPHVSRI ITDLEEDQVL MERFLDALWG

EIARRKAVCD NAGVDDAKEY

551 NSVTRMRAR GQDMALPML VVVIDEFYEW

FRIVPTADV LDSIGRQGRA

601 YWIHLMMASQ TIESRAEKL ENMGYRLVLK

ARTAGAAQAA GVPNAVNLPA

651 QAGLG YFRKS LEDVIRFQAE FLWRDYFRGV

TLDGEEQPV L VHNDYVRPQ

701 LFTNLFTPLE VSVGGPEVDA EAVFANAQEF

DEEIAEEAE GGVRTPKIGT

751 VIIDQLRRID FEPYRLWQPP LTQPVAIDDL

VNRFLGHPWQ KDYGSAARNLV

801 FPIGVDRPF KHDQPAWTVD TSGPGSNVLV

LGAGGSGKTT ALQTHCSAA

851 LTHTEQVQF YCLGYSGTAL TTV AHLPHVG

EVAGPTDPYG VRRTVAELLA

901 LVRDRKRSFL EHGASMEVF RRRKFGGELG

PVPNDGFGDV YLVIDNYRAL

951 VEENEVLIEQ VNQINQGPS FG VHVVTAD

RESELRPQVR SGFGSRVELR

1001 LAAVEDAKLV RSRFAKDV PV QSGRGMVAVN

YVRLSDPQA GLHTLVARPA

1051 LANTPANVFE SDSVAPVSR LTSQAAPPVR

RLPARFGMEQ VRERAVRDTR

1101 QGVGVGGIAW AISELDLPV YLNF AENAH

MITGRECEGR TTVLATIMSE

1151 IGRLYAPGGT SAPPTSERSA QVWLIDPRRQ

LLTMLGSNYM EKFAYNLDGV

1201 SAMVGELAA LASREPPDL SAEELLSRSW

WSGPEIFLII DDIQQLPPSF

1251 DSPLQKVVPW VTRAGDVGLH VIATRTFGGW

SSAGSDPMLR ALHQANAPLL

1301 VMDADPDEGF IRGKMKGGPL PRGRGLLMAE

DTGVLVQVAE TDMRR

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS

1 REFERENCES IN FILE CA (1967 TO DATE)

1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

=> E "SPOOJ"/CN 25

E1 1 SPONTO N 723/CN

E2 1 SPONTOX/CN

E3 0 --> SPOOJ/CN

E4 1 SPOOJ REGULATOR (SOJ) (TREPONEMA

PALLIDUM GENE TP0272)/CN

E5 1 SPOOJ REGULATOR, SOJ/PARA FAMILY

(CLOSTRIDIUM ACETOBUTYLICUM STRAIN ATCC 824 GENE
CAP0177)/CN

E6 1 SPOOM-RELATED PROTEIN (VIBRIO CHOLERAEE
STRAIN N16961 GENE VC0039)/CN

E7 1 SPOP-BL/CN

E8 1 SPOPHYLLIN RETARD/CN

E9 1 SPOR(1,3-DITHIOLANE-2,3'-

TRICYCLO(2.2.1.02,6)HEPTANE)/CN

E10 1 SPOR-KLENZ/CN

E11 1 SPORACURACIN A/CN

E12 1 SPORACURACIN B/CN

E13 1 SPORAMIN/CN

E14 1 SPORAMIN (IPOMOEAE BATAS STRAIN

TAINONG 57 PRECURSOR)/CN

E15 1 SPORAMIN (PHARMACEUTICAL)/CN

E16 1 SPORAMIN (SWEET POTATO CLONE PGEM-TIA
GENE SPTI-1 PRECURSOR)/CN

E17 1 SPORAMIN (SWEET POTATO CLONE PGEM-TIA
PRECURSOR)/CN

E18 1 SPORAMIN (SWEET POTATO)/CN

E19 1 SPORAMIN A (SWEET POTATO CLONE GSPO-A1
REDUCED)/CN

E20 1 SPORAMIN A (SWEET POTATO CLONE PIMO23
REDUCED)/CN

E21 1 SPORAMIN A (SWEET POTATO STRAIN NANSHU-
88)/CN

E22 1 SPORAMIN A 2 (SWEET POTATO CLONE PIMO335
REDUCED)/CN

E23 1 SPORAMIN A 2, PREPRO- (SWEET POTATO CLONE
PIMO335 REDUCED)/CN

E24 1 SPORAMIN A 2, PRO- (SWEET POTATO CLONE
PIMO335 REDUCED)/CN

E25 1 SPORAMIN A, PREPRO- (SWEET POTATO CLONE
GSPO-A1 REDUCED)/CN

=> S E4

L2 1 "SPOOJ REGULATOR (SOJ) (TREPONEMA PALLIDUM
GENE TP0272)"/CN

=> DIS L2 1 SQIDE

THE ESTIMATED COST FOR THIS REQUEST IS 5.53 U.S.
DOLLARS

DO YOU WANT TO CONTINUE WITH THIS REQUEST? (Y)/N:Y

L2 ANSWER 1 OF 1 REGISTRY COPYRIGHT 2002 ACS

RN 209603-85-0 REGISTRY

CN SpoOJ regulator (soj) (Treponema pallidum gene TP0272)
(9CI)

(CA INDEX NAME)

OTHER NAMES:

CN GenBank AE001208-derived protein GI 3322545

FS PROTEIN SEQUENCE

SQL 253

SEQ 1 MGKTLVFNQ KGGVGKTTSA INLGAYLALA

GKKTLLVDFD PQGNMSSGLG

51 LARGLTVYDL LAGKAHINSV LRTTPVHNLF

AIPASIDLSG ATVELVDEQD

101 RELYLKKILA EVKDTYDFIL IDCPPSLGIL

TLNGLAAANE VFIPLQCEYF

151 ALEGLTLLQ TVKRVQSGLN TALSIGGIF

F1	27	BIOSIS
F2	19	CAPLUS

F3 16 BIOTECHNO
 F4 15 EMBASE
 F5 13 LIFESCI
 F6 13 SCISEARCH
 F7 11 GENBANK
 F8 10 ESBIOBASE
 F9 10 MEDLINE
 F10 9 USPATFULL
 F11 8 TOXCENTER
 F12 4 BIOTECHABS
 F13 4 BIOTECHDS
 F14 2 IFIPAT
 F15 2 PASCAL
 F16 2 WPIDS
 F17 2 WPINDEX
 F18 1 CABA
 F19 1 FEDRIP
 F20 1 FSTA
 F21 1 JICST-EPLUS

=> FILE BIOSIS CAPLUS
 COST IN U.S. DOLLARS
 ENTRY SESSION
 FULL ESTIMATED COST 1.59 23.73

FILE 'BIOSIS' ENTERED AT 12:55:42 ON 24 MAY 2002
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=> S SPOIIIIE
 L5 97 SPOIIIIE

=> S SPOOJ
 L6 46 SPOOJ

=> S L5 AND L6
 L7 3 L5 AND L6

=> DUP REM L7
 PROCESSING COMPLETED FOR L7
 L8 3 DUP REM L7 (0 DUPLICATES REMOVED)

=> D TI SO 1-3

L8 ANSWER 1 OF 3 BIOSIS COPYRIGHT 2002 BIOLOGICAL
 ABSTRACTS INC.
 TI Bacillus strain and antibiotic screening method.
 SO Official Gazette of the United States Patent and Trademark Office
 Patents,
 (Feb. 26, 2002) Vol. 1255, No. 4, pp. No Pagination.
<http://www.uspto.gov/web/menu/patdata.html>. e-file.
 ISSN: 0098-1133.

L8 ANSWER 2 OF 3 CAPLUS COPYRIGHT 2002 ACS
 TI Synthetic lethal phenotypes caused by mutations affecting
 chromosome
 partitioning in Bacillus subtilis
 SO Journal of Bacteriology (1999), 181(18), 5860-5864
 CODEN: JOBAAY; ISSN: 0021-9193

L8 ANSWER 3 OF 3 CAPLUS COPYRIGHT 2002 ACS
 TI Mutant Bacillus strain and antibiotic screening method
 SO PCT Int. Appl., 16 pp.
 CODEN: PIXXD2

=> D IBIB AB 2

L8 ANSWER 2 OF 3 CAPLUS COPYRIGHT 2002 ACS
 ACCESSION NUMBER: 1999:616178 CAPLUS
 DOCUMENT NUMBER: 132:920
 TITLE: Synthetic lethal phenotypes caused by mutations
 affecting chromosome partitioning in Bacillus subtilis
 AUTHOR(S): Britton, Robert A.; Grossman, Alan D.
 CORPORATE SOURCE: Department of Biology, Massachusetts
 Institute of
 Technology, Cambridge, MA, 02139, USA
 SOURCE: Journal of Bacteriology (1999), 181(18), 5860-
 5864
 CODEN: JOBAAY; ISSN: 0021-9193
 PUBLISHER: American Society for Microbiology
 DOCUMENT TYPE: Journal
 LANGUAGE: English
 AB We investigated the genetic interactions between mutations
 affecting
 chromosome structure and partitioning in Bacillus subtilis.
 Loss-of-function mutations in *spoIIIIE* (encoding a putative DNA
 translocase) and *smc* (involved in chromosome structure and
 partitioning)
 caused a synthetic lethal phenotype. We constructed a conditional
 mutation in *smc* and found that many of the *spoIIIIE smc*
 double-mutant cells had a chromosome bisected by a division
 septum. The
 growth defect of the double mutant was exacerbated by a null
 mutation in
 the chromosome partitioning gene *spo0J*. These results suggest that
 mutants defective in nucleoid structure are unable to move
 chromosomes out
 of the way of the invaginating septum and that *SpoIIIIE* is
 involved in repositioning these bisected chromosomes during
 vegetative
 growth.
 REFERENCE COUNT: 31 THERE ARE 31 CITED
 REFERENCES AVAILABLE FOR THIS
 RECORD. ALL CITATIONS AVAILABLE IN THE
 RE FORMAT

=> D HIS

(FILE 'HOME' ENTERED AT 12:48:41 ON 24 MAY 2002)

FILE 'REGISTRY' ENTERED AT 12:49:49 ON 24 MAY 2002
 E "SPOIIIIE"/CN 25
 L1 1 S E4
 E "SPOOJ"/CN 25
 L2 1 S E4

INDEX 'ADISALERTS, ADISINSIGHT, ADISNEWS,
 AGRICOLA, ANABSTR, AQUASCI,
 BIOBUSINESS, BIOCOMMERCE, BIOSIS, BIOTECHABS,
 BIOTECHDS, BIOTECHNO, CABA,
 CANCERLIT, CAPLUS, CEABA-VTB, CEN, CIN, CONFSCI,
 CROPB, CROPU, DDFB,
 DDFU, DGENE, DRUGB, DRUGLAUNCH, DRUGMONOG2, ...'
 ENTERED AT 12:53:52 ON
 24 MAY 2002

SEA SPOIIIIE

 1 FILE AQUASCI
 47 FILE BIOSIS
 6 FILE BIOTECHABS
 6 FILE BIOTECHDS
 28 FILE BIOTECHNO
 1 FILE CABA
 50 FILE CAPLUS
 1 FILE CEABA-VTB
 1 FILE CONFSCI
 6 FILE DGENE
 30 FILE EMBASE
 23 FILE ESBIOBASE
 3 FILE FSTA

54 FILE GENBANK
 8 FILE IFIPAT
 5 FILE JICST-EPLUS
 34 FILE LIFESCI
 37 FILE MEDLINE
 9 FILE PASCAL
 2 FILE PROMT
 34 FILE SCISEARCH
 8 FILE TOXCENTER
 17 FILE USPATFULL
 5 FILE WPIDS
 5 FILE WPINDEX
 L3 QUE SPOIIIIE

 SEA SPOOJ

 27 FILE BIOSIS
 4 FILE BIOTECHABS
 4 FILE BIOTECHDS
 16 FILE BIOTECHNO
 1 FILE CABA
 19 FILE CAPLUS
 15 FILE EMBASE
 10 FILE ESBIODASE
 1 FILE FEDRIP
 1 FILE FSTA
 11 FILE GENBANK
 2 FILE IFIPAT
 1 FILE JICST-EPLUS
 13 FILE LIFESCI
 10 FILE MEDLINE
 2 FILE PASCAL
 13 FILE SCISEARCH
 8 FILE TOXCENTER
 9 FILE USPATFULL
 2 FILE WPIDS
 2 FILE WPINDEX
 L4 QUE SPOOJ

 FILE 'BIOSIS, CAPLUS' ENTERED AT 12:55:42 ON 24 MAY 2002
 L5 97 S SPOIIIIE
 L6 46 S SPOOJ
 L7 3 S L5 AND L6
 L8 3 DUP REM L7 (0 DUPLICATES REMOVED)

 => LOG HOLD

COST IN U.S. DOLLARS	ENTRY	SINCE FILE	SESSION	TOTAL
FULL ESTIMATED COST		13.14		36.87

 DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)

SINCE FILE	TOTAL	ENTRY	SESSION
CA SUBSCRIBER PRICE		-0.62	-0.62

 SESSION WILL BE HELD FOR 60 MINUTES
 STN INTERNATIONAL SESSION SUSPENDED AT 12:59:50 ON 24 MAY 2002

 Connecting via Winsock to STN

 Welcome to STN International! Enter x:x

 LOGINID:SSSPTA1636DXS

 PASSWORD:
 ***** RECONNECTED TO STN INTERNATIONAL *****
 SESSION RESUMED IN FILE 'BIOSIS, CAPLUS' AT 13:26:13 ON 24 MAY 2002
 FILE 'BIOSIS' ENTERED AT 13:26:13 ON 24 MAY 2002

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 FILE 'CAPLUS' ENTERED AT 13:26:13 ON 24 MAY 2002
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COST IN U.S. DOLLARS	ENTRY	SINCE FILE	SESSION	TOTAL
FULL ESTIMATED COST		13.14		36.87

 DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)

SINCE FILE	TOTAL	ENTRY	SESSION
CA SUBSCRIBER PRICE		-0.62	-0.62

 => FILE MEDLINE CAPLUS BIOSIS

COST IN U.S. DOLLARS	ENTRY	SINCE FILE	SESSION	TOTAL
FULL ESTIMATED COST		13.14		36.87

 DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)

SINCE FILE	TOTAL	ENTRY	SESSION
CA SUBSCRIBER PRICE		-0.62	-0.62

 FILE 'MEDLINE' ENTERED AT 13:26:26 ON 24 MAY 2002

 FILE 'CAPLUS' ENTERED AT 13:26:26 ON 24 MAY 2002
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 => S REPORTER GENE
 L9 45878 REPORTER GENE

 => S COMPLEMENTA?
 L10 317475 COMPLEMENTA?

 => S L9 AND L10
 L11 2166 L9 AND L10

 => S L9(P)L10
 L12 822 L9(P) L10

 => S SIGMA FACTOR
 L13 6401 SIGMA FACTOR

 => S SIGMA F
 L14 2900 SIGMA F

 => S L12 AND L14
 L15 0 L12 AND L14

 => DUP REM L12
 PROCESSING COMPLETED FOR L12
 L16 400 DUP REM L12 (422 DUPLICATES REMOVED)

 => D TI 1-10

 L16 ANSWER 1 OF 400 CAPLUS COPYRIGHT 2002 ACS
 TI Crucifer tobamovirus vector containing internal ribosome entry sites for
 cap-independent translation of heterologous genes in transgenic plants

 L16 ANSWER 2 OF 400 CAPLUS COPYRIGHT 2002 ACS
 TI Rat and human genes for a novel mammalian biogenic amine receptor and
 their use in the development of therapeutics

 L16 ANSWER 3 OF 400 CAPLUS COPYRIGHT 2002 ACS
 TI PCR primers for construction of transcription template for dilution

batch-type cell-free protein synthesis system

L16 ANSWER 4 OF 400 CAPLUS COPYRIGHT 2002 ACS

TI The promoter of Ls (Lateral suppressor) gene of tomato regulating side-shoot, petal and abscission zone formation and its use in development of new plant varieties

L16 ANSWER 5 OF 400 CAPLUS COPYRIGHT 2002 ACS

TI Nucleic acid libraries in adenoviral-derived gene expression vectors and their use for high throughput screening and functional genomics

L16 ANSWER 6 OF 400 CAPLUS COPYRIGHT 2002 ACS

TI Targeted inhibition of gene expression with double-stranded RNA with single-stranded ends

L16 ANSWER 7 OF 400 MEDLINE DUPLICATE 1

TI Transcriptionally active polymerase chain reaction (TAP): high throughput gene expression using genome sequence data.

L16 ANSWER 8 OF 400 MEDLINE DUPLICATE 2

TI Pseudomonas aeruginosa displays multiple phenotypes during development as a biofilm.

L16 ANSWER 9 OF 400 MEDLINE DUPLICATE 3

TI Characterization of the norB gene, encoding nitric oxide reductase, in the nondenitrifying cyanobacterium Synechocystis sp. strain PCC6803.

L16 ANSWER 10 OF 400 BIOSIS COPYRIGHT 2002

BIOLOGICAL ABSTRACTS INC.

TI Smooth muscle-specific transcription without a CA₁G box element.

=> FILE REGISTRY

COST IN U.S. DOLLARS	SINCE FILE	TOTAL
	ENTRY	SESSION
FULL ESTIMATED COST	17.91	54.78

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)

SINCE FILE	TOTAL	
	ENTRY	SESSION
CA SUBSCRIBER PRICE	0.00	-0.62

FILE 'REGISTRY' ENTERED AT 13:31:57 ON 24 MAY 2002

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STRUCTURE FILE UPDATES: 22 MAY 2002 HIGHEST RN 420781-77-7

DICTIONARY FILE UPDATES: 22 MAY 2002 HIGHEST RN 420781-77-7

TSCA INFORMATION NOW CURRENT THROUGH July 7, 2001

Please note that search-term pricing does apply when conducting SmartSELECT searches.

Crossover limits have been increased. See HELP CROSSOVER for details.

Calculated physical property data is now available. See HELP PROPERTIES

for more information. See STNote 27, Searching Properties in the CAS Registry File, for complete details:

<http://www.cas.org/ONLINE/STN/STNOTES/stnotes27.pdf>

=> E "PROKARYOTE"/CN 25

E1 1 PROKAOLINITE/CN

E2 1 PROKARBOL/CN

E3 0 --> PROKARYOTE/CN

E4 1 PROKARYOTIC LEADER PEPTIDASE/CN

E5 1 PROKARYOTIC SIGNAL PEPTIDASE/CN

E6 1 PROKARYOTIC SIGNAL PROTEINASE/CN

E7 1 PROKARYOTIC TELOMERASE/CN

E8 1 PROKARYOTIC TYPE I SIGNAL PEPTIDASE

(AGROBACTERIUM TUMEFACIENS STRAIN C58 GENE SIPP)/CN

E9 1 PROKAYVIT/CN

E10 1 PROKAYVIT ORAL/CN

E11 1 PROKETAZINE/CN

E12 1 PROKETAZINE MALEATE/CN

E13 1 PROKEXIN/CN

E14 1 PROKHINOR/CN

E15 1 PROKHINOR 2558/CN

E16 1 PROKHINOR 2948/CN

E17 1 PROKHINOR GR 77/CN

E18 1 PROKINE/CN

E19 1 PROKINETICIN 1 (HUMAN GENE PROK1

PRECURSOR)/CN

E20 1 PROKINETICIN 2 (HUMAN GENE PROK2

PRECURSOR)/CN

E21 1 PROKLAMILIN/CN

E22 1 PROKRON 1/CN

E23 1 PROKRON 10/CN

E24 1 PROKRON 10L/CN

E25 1 PROKRON 11/CN

=> E "BACTERIUM"/CN 25

E1 1 BACTERIOVIRIDIN/CN

E2 1 BACTERIOVIRIDINE/CN

E3 0 --> BACTERIUM/CN

E4 1 BACTERIUM ACIDOPHILUM/CN

E5 1 BACTERIUM BULGARICUM/CN

E6 1 BACTERIUM COLI/CN

E7 1 BACTERIUM PRODIGIOSUM/CN

E8 1 BACTERIUM PYOCYANEUM/CN

E9 1 BACTERIUM SUBTILIS/CN

E10 1 BACTERIUM SUPESTIFER/CN

E11 1 BACTERIUM TABACUM/CN

E12 1 BACTEROCIN TRANSPORT ACCESSORY PROTEIN

(STREPTOCOCCUS PNEUMONIAE STRAIN TIGR4 GENE

SP1499)/CN

E13 1 BACTEROID DEVELOPMENT PROTEIN

(AGROBACTERIUM TUMEFACIENS STRAIN C58 GENE

BACA)/CN

E14 1 BACTEROID DEVELOPMENT PROTEIN BACA

(BRUCELLA MELITENSIS STRAIN 16M GENE BME11553)/CN

E15 1 BACTEROIDES GINGIVALIS SERINE

PROTEINASE/CN

E16 1 BACTEROIDES NODOSUS SERINE

PROTEINASE/CN

E17 1 BACTERON B 6/CN

E18 1 BACTEROPLANECIN/CN

E19 1 BACTESID/CN

E20 1 BACTI-STAT SOAP/CN

E21 1 BACTIFLUDRON/CN

E22 1 BACTIFOLISTOP/CN

E23 1 BACTIFOLISTOP L/CN

E24 1 BACTIGRAS/CN

E25 1 BACTIL SC/CN

=> FILE MEDLINE BIOSIS CAPLUS

COST IN U.S. DOLLARS	SINCE FILE	TOTAL
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FULL ESTIMATED COST	0.76	55.54

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)

SINCE FILE	TOTAL	
	ENTRY	SESSION
CA SUBSCRIBER PRICE	0.00	-0.62

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=> S L16
L17 400 L16

=> S SUBTILIS
L18 70987 SUBTILIS

=> S L17 AND L18
L19 4 L17 AND L18

=> D TI 1-4

L19 ANSWER 1 OF 4 MEDLINE
TI A *Bacillus subtilis* gene induced by cold shock encodes a
membrane phospholipid desaturase.

L19 ANSWER 2 OF 4 MEDLINE
TI Regulation of the *Bacillus subtilis* pyrimidine biosynthetic
(pyr) gene cluster by an autogenous transcriptional attenuation
mechanism.

L19 ANSWER 3 OF 4 MEDLINE
TI Shuttle vectors containing a multiple cloning site and a lacZ alpha
gene
for conjugal transfer of DNA from *Escherichia coli* to gram-positive
bacteria.

L19 ANSWER 4 OF 4 CAPLUS COPYRIGHT 2002 ACS
TI The *aarC* gene involved in the regulation of 2'-N-acetyltransferase
activity in *Providencia* and its use in screening for novel
antimicrobial
agents

=> D TI SO 1-4

L19 ANSWER 1 OF 4 MEDLINE
TI A *Bacillus subtilis* gene induced by cold shock encodes a
membrane phospholipid desaturase.
SO JOURNAL OF BACTERIOLOGY, (1998 Apr) 180 (8) 2194-200.
Journal code: HH3; 2985120R. ISSN: 0021-9193.

L19 ANSWER 2 OF 4 MEDLINE
TI Regulation of the *Bacillus subtilis* pyrimidine biosynthetic
(pyr) gene cluster by an autogenous transcriptional attenuation
mechanism.
SO JOURNAL OF BACTERIOLOGY, (1994 Jun) 176 (12) 3708-22.
Journal code: HH3; 2985120R. ISSN: 0021-9193.

L19 ANSWER 3 OF 4 MEDLINE
TI Shuttle vectors containing a multiple cloning site and a lacZ alpha
gene
for conjugal transfer of DNA from *Escherichia coli* to gram-positive
bacteria.
SO GENE, (1991 Jun 15) 102 (1) 99-104.
Journal code: FOP; 7706761. ISSN: 0378-1119.

L19 ANSWER 4 OF 4 CAPLUS COPYRIGHT 2002 ACS
TI The *aarC* gene involved in the regulation of 2'-N-acetyltransferase
activity in *Providencia* and its use in screening for novel
antimicrobial
agents
SO PCT Int. Appl., 86 pp.
CODEN: PIXXD2

=> D IBIB AB 2-4

L19 ANSWER 2 OF 4 MEDLINE
ACCESSION NUMBER: 94266724 MEDLINE
DOCUMENT NUMBER: 94266724 PubMed ID: 8206849
TITLE: Regulation of the *Bacillus subtilis* pyrimidine
biosynthetic (pyr) gene cluster by an autogenous
transcriptional attenuation mechanism.
AUTHOR: Turner R J; Lu Y; Switzer R L
CORPORATE SOURCE: Department of Biochemistry, University of
Illinois, Urbana
61801.
CONTRACT NUMBER: GM47112 (NIGMS)
SOURCE: JOURNAL OF BACTERIOLOGY, (1994 Jun) 176
(12) 3708-22.
Journal code: HH3; 2985120R. ISSN: 0021-9193.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-M59757
ENTRY MONTH: 199407
ENTRY DATE: Entered STN: 19940721
Last Updated on STN: 19940721
Entered Medline: 19940714

AB A complete transcript of the *Bacillus subtilis* pyr operon
contains the following elements in 5' to 3' order: a 151-nucleotide (nt)
untranslated leader; pyrR, encoding a 20-kDa protein; a 173-nt
intercistronic region; pyrP, encoding a 46-kDa protein; a 145-nt
intercistronic region; and eight overlapping cistrons encoding all of
the
six enzymes for de novo pyrimidine biosynthesis. Transcription is
controlled by the availability of pyrimidines via an attenuation
mechanism. There are three transcription terminators within the
operon,
each of which is preceded by another stem-loop structure, the
antiterminator, whose formation would prevent formation of the
terminator
stem-loop. These are located in the leader, the pyrR-pyrP
intercistronic
region, and the pyrP-pyrB intercistronic region. Northern (RNA) blot
analysis has identified transcripts of lengths which coincide with
termination at these proposed attenuation sites and whose relative
abundances vary in the expected pyrimidine-dependent manner. Each
antiterminator contains a 50-base conserved sequence in its
promoter-proximal half. Various transcriptional fusions of the pyr
promoter and surrounding sequences to promoterless reporter
genes support an attenuation mechanism whereby when pyrimidines
are abundant, the PyrR protein binds to the conserved sequence in the
pyr
mRNA and disrupts the antiterminator, permitting terminator hairpin
formation and promoting transcription termination. Deletion of pyrR
from
the chromosome resulted in the constitutive, elevated expression of
aspartate transcarbamylase, which is encoded by pyrB, the third gene
in
the operon. **Complementation** of an *E. coli* upp mutant, as well as
direct enzymatic assay, has demonstrated that pyrR also confers
uracil
phosphoribosyltransferase activity. Analysis of pyrR and upp deletion
mutants demonstrated that upp, not pyrR, encodes the quantitatively
important uracil phosphoribosyltransferase activity. The pyrP gene
probably encodes an integral membrane uracil permease.

L19 ANSWER 3 OF 4 MEDLINE
ACCESSION NUMBER: 91323739 MEDLINE
DOCUMENT NUMBER: 91323739 PubMed ID: 1864514
TITLE: Shuttle vectors containing a multiple cloning site and a
lacZ alpha gene for conjugal transfer of DNA from
Escherichia coli to gram-positive bacteria.
AUTHOR: Trieu-Cuot P; Carlier C; Poyart-Salmeron C;
Courvalin P

CORPORATE SOURCE: Unite des Agents Antibacteriens, CNRS UA 271, Institut

Pasteur, France.

SOURCE: GENE, (1991 Jun 15) 102 (1) 99-104.

Journal code: FOP; 7706761. ISSN: 0378-1119.

PUB. COUNTRY: Netherlands

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 199109

ENTRY DATE: Entered STN: 19910929

Last Updated on STN: 19910929

Entered Medline: 19910909

AB The mobilizable shuttle cloning vectors, pAT18 and pAT19, are composed of:

(i) the replication origins of pUC and of the broad-host-range enterococcal plasmid pAM beta 1; (ii) an erythromycin-resistance-encoding gene expressed in Gram- and Gram+ bacteria; (iii) the transfer origin of the IncP plasmid RK2; and (iv) the multiple cloning site and the lacZ alpha reporter gene of pUC18 (pAT18) and pUC19 (pAT19). These 6.6-kb plasmids contain ten unique cloning sites that allow screening of derivatives containing DNA inserts by alpha-complementation in Escherichia coli carrying the lacZ delta M15 deletion, and can be efficiently mobilized by self-transferable IncF plasmids co-resident in the E. coli donors. Plasmids pAT18, pAT19 and recombinant derivatives have been successfully transferred by conjugation from E. coli to Bacillus subtilis, Bacillus thuringiensis, Listeria monocytogenes, Enterococcus faecalis, Lactococcus lactis, and Staphylococcus aureus at frequencies ranging from 10(-6) to 10(-9). The presence of a restriction system in the recipient dramatically affects (by three orders of magnitude) the efficiency of conjugal transfer of these vectors from E. coli to Gram+ bacteria.

L19 ANSWER 4 OF 4 CAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 1998:672694 CAPLUS

DOCUMENT NUMBER: 129:272926

TITLE: The aarC gene involved in the regulation of 2'-N-acetyltransferase activity in Providencia and its use in screening for novel antimicrobial agents

INVENTOR(S): Rather, Philip N.

PATENT ASSIGNEE(S): Case Western Reserve University, USA

SOURCE: PCT Int. Appl., 86 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9842875	A1	19981001	WO 1998-US6061	19980327
W: AU, CA, JP				
RW: AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
US 5858367	A	19990112	US 1997-827190	19970327
AU 9865890	A1	19981020	AU 1998-65890	19980327
EP 975801	A1	20000202	EP 1998-912092	19980327
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
JP 2001523097	T2	20011120	JP 1998-546016	19980327
US 6383745	B1	20020507	US 1998-170187	19981013
PRIORITY APPLN. INFO.: US 1997-827190 A 19970327				
WO 1998-US6061 W 19980327				

AB The aarC gene that plays a role of the regulation of the synthesis of a

key enzyme in peptidoglycan biosynthesis, the 2'-N-acetyltransferase encoded by the aac(2')-Ia gene, and that is essential for the viability of bacteria is cloned and characterized. The gene regulates expression of the aac(2')-Ia gene in response to cell d. Using a reporter gene under control of the aac(2')-Ia promoter can therefore be used to measure cell growth and the bacteriostatic and antibiotic effects of test compds. A reporter gene system using the promoter of the aac(2')-Ia gene to measure inhibition of aarC function is described for use in screening antibiotics. The gene may also be used as a target in the diagnosis of infection. Cloning of the aarC gene by complementation is described.

=> LOG HOLD

COST IN U.S. DOLLARS	ENTRY	SINCE FILE	TOTAL
FULL ESTIMATED COST		13.63	69.17

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SINCE FILE	TOTAL	ENTRY	SESSION
CA SUBSCRIBER PRICE		-0.62	-1.24

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FILE 'MEDLINE' ENTERED AT 14:03:32 ON 24 MAY 2002
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COST IN U.S. DOLLARS	ENTRY	SINCE FILE	TOTAL
FULL ESTIMATED COST		13.63	69.17

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)

SINCE FILE	TOTAL	ENTRY	SESSION
CA SUBSCRIBER PRICE		-0.62	-1.24

=> D HIS

(FILE 'HOME' ENTERED AT 12:48:41 ON 24 MAY 2002)

FILE 'REGISTRY' ENTERED AT 12:49:49 ON 24 MAY 2002
E "SPOIII"/CN 25
L1 1 S E4
E "SPOOJ"/CN 25
L2 1 S E4

INDEX 'ADISALERTS, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, AQUASCI, BIOBUSINESS, BIOCOMMERCE, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CANCERLIT, CAPLUS, CEABA-VTB, CEN, CIN, CONFSCI,

CROPB, CROPU, DDFB,
DDFU, DGENE, DRUGB, DRUGLAUNCH, DRUGMONOG2, ...'
ENTERED AT 12:53:52 ON

24 MAY 2002

SEA SPOIIE

1 FILE AQUASCI
47 FILE BIOSIS
6 FILE BIOTECHABS
6 FILE BIOTECHDS
28 FILE BIOTECHNO
1 FILE CABA
50 FILE CAPLUS
1 FILE CEABA-VTB
1 FILE CONFSCI
6 FILE DGENE
30 FILE EMBASE
23 FILE ESBIODASE
3 FILE FSTA
54 FILE GENBANK
8 FILE IFIPAT
5 FILE JICST-EPLUS
34 FILE LIFESCI
37 FILE MEDLINE
9 FILE PASCAL
2 FILE PROMT
34 FILE SCISEARCH
8 FILE TOXCENTER
17 FILE USPATFULL
5 FILE WPIDS
5 FILE WPINDEX
L3 QUE SPOIIE

SEA SPOOJ

27 FILE BIOSIS
4 FILE BIOTECHABS
4 FILE BIOTECHDS
16 FILE BIOTECHNO
1 FILE CABA
19 FILE CAPLUS
15 FILE EMBASE
10 FILE ESBIODASE
1 FILE FEDRIP
1 FILE FSTA
11 FILE GENBANK
2 FILE IFIPAT
1 FILE JICST-EPLUS
13 FILE LIFESCI
10 FILE MEDLINE
2 FILE PASCAL
13 FILE SCISEARCH
8 FILE TOXCENTER
9 FILE USPATFULL
2 FILE WPIDS
2 FILE WPINDEX
L4 QUE SPOOJ

FILE 'BIOSIS, CAPLUS' ENTERED AT 12:55:42 ON 24 MAY
2002

L5 97 S SPOIIE
L6 46 S SPOOJ
L7 3 S L5 AND L6
L8 3 DUP REM L7 (0 DUPLICATES REMOVED)

FILE 'MEDLINE, CAPLUS, BIOSIS' ENTERED AT 13:26:26 ON
24 MAY 2002

L9 45878 S REPORTER GENE
L10 317475 S COMPLEMENTA?
L11 2166 S L9 AND L10
L12 822 S L9(P)L10
L13 6401 S SIGMA FACTOR
L14 2900 S SIGMA F

L15 0 S L12 AND L14
L16 400 DUP REM L12 (422 DUPLICATES REMOVED)

FILE 'REGISTRY' ENTERED AT 13:31:57 ON 24 MAY 2002
E "PROKARYOTE"/CN 25
E "BACTERIUM"/CN 25

FILE 'MEDLINE, BIOSIS, CAPLUS' ENTERED AT 13:33:15 ON
24 MAY 2002

L17 400 S L16
L18 70987 S SUBTILIS
L19 4 S L17 AND L18

=> S COMPLEMENT?
L20 556256 COMPLEMENT?

=> S FUNCTION?
L21 3739694 FUNCTION?

=> S L2O(W)L21
L22 0 L2O(W) L21

=> S L2O(A)L21
L23 4121 L2O(A) L21

=> S L18 AND L23
L24 106 L18 AND L23

=> DUP REM L24
PROCESSING COMPLETED FOR L24
L25 46 DUP REM L24 (60 DUPLICATES REMOVED)

=> D TI 1-10

L25 ANSWER 1 OF 46 CAPLUS COPYRIGHT 2002 ACS
TI Hansenula HARO7 gene and encoded chorismate mutase and its use
as a
selectable marker

L25 ANSWER 2 OF 46 CAPLUS COPYRIGHT 2002 ACS
TI Lumazine synthase and riboflavin synthase genes from plants and
Magnaporthe grisea

L25 ANSWER 3 OF 46 CAPLUS COPYRIGHT 2002 ACS
TI Lumazine synthase and riboflavin synthase from plants and fungi

L25 ANSWER 4 OF 46 CAPLUS COPYRIGHT 2002 ACS
TI Lumazine synthase and riboflavin synthase and their genes from
plants and
fungi

L25 ANSWER 5 OF 46 MEDLINE DUPLICATE 1
TI Nitrate assimilation genes of the marine diazotrophic, filamentous
cyanobacterium Trichodesmium sp. strain WH9601.

L25 ANSWER 6 OF 46 MEDLINE DUPLICATE 2
TI Characterization of OpuA, a glycine-betaine uptake system of
Lactococcus
lactis.

L25 ANSWER 7 OF 46 MEDLINE DUPLICATE 3
TI Nucleotide sequence, expression and transcriptional analysis of the
Bifidobacterium longum MB 219 lacZ gene.

L25 ANSWER 8 OF 46 MEDLINE DUPLICATE 4
TI Plant riboflavin biosynthesis. Cloning, chloroplast localization,
expression, purification, and partial characterization of spinach
lumazine
synthase.

L25 ANSWER 9 OF 46 MEDLINE DUPLICATE 5
TI Identification and disruption of BetL, a secondary glycine betaine
transport system linked to the salt tolerance of Listeria
monocytogenes

LO28.

L25 ANSWER 10 OF 46 MEDLINE DUPLICATE 6
TI Staphylokinase as a plasminogen activator component in recombinant fusion proteins.

=> S L25 NOT PY>1998

L26 36 L25 NOT PY>1998

=> D TI SO 1-36

L26 ANSWER 1 OF 36 MEDLINE
TI Mutations in *Bartonella bacilliformis* gyrB confer resistance to coumermycin A1.
SO ANTIMICROBIAL AGENTS AND CHEMOTHERAPY, (1998 Nov) 42 (11) 2906-13.
Journal code: 6HK; 0315061. ISSN: 0066-4804.

L26 ANSWER 2 OF 36 MEDLINE
TI Basic and acidic regions flanking the HMG domain of maize HMGa modulate the interactions with DNA and the self-association of the protein.
SO BIOCHEMISTRY, (1998 Feb 24) 37 (8) 2673-81.
Journal code: A0G; 0370623. ISSN: 0006-2960.

L26 ANSWER 3 OF 36 MEDLINE
TI Characterization of *Bacillus subtilis* hemN.
SO JOURNAL OF BACTERIOLOGY, (1997 Nov) 179 (22) 7181-5.
Journal code: HH3; 2985120R. ISSN: 0021-9193.

L26 ANSWER 4 OF 36 MEDLINE
TI Synthesis of the osmoprotectant glycine betaine in *Bacillus subtilis*: characterization of the gbsAB genes.
SO JOURNAL OF BACTERIOLOGY, (1996 Sep) 178 (17) 5121-9.
Journal code: HH3; 2985120R. ISSN: 0021-9193.

L26 ANSWER 5 OF 36 MEDLINE
TI Three transport systems for the osmoprotectant glycine betaine operate in *Bacillus subtilis*: characterization of OpuD.
SO JOURNAL OF BACTERIOLOGY, (1996 Sep) 178 (17) 5071-9.
Journal code: HH3; 2985120R. ISSN: 0021-9193.

L26 ANSWER 6 OF 36 MEDLINE
TI Cloning and characterization of the yeast HEM14 gene coding for protoporphyrinogen oxidase, the molecular target of diphenyl ether-type herbicides.
SO JOURNAL OF BIOLOGICAL CHEMISTRY, (1996 Apr 12) 271 (15) 9120-8.
Journal code: HIV; 2985121R. ISSN: 0021-9258.

L26 ANSWER 7 OF 36 MEDLINE
TI A pAO1-encoded molybdopterine cofactor gene (moaA) of *Arthrobacter nicotinovorans*: characterization and site-directed mutagenesis of the encoded protein.
SO ARCHIVES OF MICROBIOLOGY, (1995 Aug) 164 (2) 142-51.
Journal code: 7YN; 0410427. ISSN: 0302-8933.

L26 ANSWER 8 OF 36 MEDLINE
TI Functional analysis of the *Bacillus subtilis* purT gene encoding formate-dependent-glycinamide ribonucleotide transformylase.
SO MICROBIOLOGY, (1995 Sep) 141 (Pt 9) 2211-8.
Journal code: BXW; 9430468. ISSN: 1350-0872.

L26 ANSWER 9 OF 36 MEDLINE
TI Functional characterization of the *Staphylococcus carnosus* SecA protein in *Escherichia coli* and *Bacillus subtilis* secA mutant strains.
SO FEMS MICROBIOLOGY LETTERS, (1995 Sep 15) 131 (3) 271-7.

Journal code: FML; 7705721. ISSN: 0378-1097.

L26 ANSWER 10 OF 36 MEDLINE
TI The *Saccharomyces cerevisiae* RIB4 gene codes for 6,7-dimethyl-8-ribityllumazine synthase involved in riboflavin biosynthesis.
Molecular characterization of the gene and purification of the encoded protein.
SO JOURNAL OF BIOLOGICAL CHEMISTRY, (1995 Oct 6) 270 (40) 23801-7.
Journal code: HIV; 2985121R. ISSN: 0021-9258.

L26 ANSWER 11 OF 36 MEDLINE
TI A new *Bradyrhizobium japonicum* gene required for free-living bacteroid development is conserved in other bacteria and in plants.
SO MOLECULAR PLANT-MICROBE INTERACTIONS, (1995 May-Jun) 8 (3) 454-64.
Journal code: A9P; 9107902. ISSN: 0894-0282.

L26 ANSWER 12 OF 36 MEDLINE
TI Isolation of cDNAs encoding GTP cyclohydrolase II from *Arabidopsis thaliana*.
SO GENE, (1995 Jul 28) 160 (2) 303-4.
Journal code: FOP; 7706761. ISSN: 0378-1119.

L26 ANSWER 13 OF 36 MEDLINE
TI OpuA, an osmotically regulated binding protein-dependent transport system for the osmoprotectant glycine betaine in *Bacillus subtilis*.
SO JOURNAL OF BIOLOGICAL CHEMISTRY, (1995 Jul 14) 270 (28) 16701-13.
Journal code: HIV; 2985121R. ISSN: 0021-9258.

L26 ANSWER 14 OF 36 MEDLINE
TI Structural comparison of the histidine-containing phosphocarrier protein HPr.
SO BIOCHEMISTRY AND CELL BIOLOGY, (1994 May-Jun) 72 (5-6) 202-17.
Journal code: ALR; 8606068. ISSN: 0829-8211.

L26 ANSWER 15 OF 36 MEDLINE
TI Riboflavin biosynthesis in *Saccharomyces cerevisiae*. Cloning, characterization, and expression of the RIB5 gene encoding riboflavin synthase.
SO JOURNAL OF BIOLOGICAL CHEMISTRY, (1995 Jan 6) 270 (1) 437-44.
Journal code: HIV; 2985121R. ISSN: 0021-9258.

L26 ANSWER 16 OF 36 MEDLINE
TI Cloning and nucleotide sequence of *Pseudomonas aeruginosa* DNA gyrase gyrA gene from strain PAO1 and quinolone-resistant clinical isolates.
SO ANTIMICROBIAL AGENTS AND CHEMOTHERAPY, (1994 Sep) 38 (9) 1944-52.
Journal code: 6HK; 0315061. ISSN: 0066-4804.

L26 ANSWER 17 OF 36 MEDLINE
TI Clustering and co-transcription of the *Bacillus subtilis* genes encoding the aminoacyl-tRNA synthetases specific for glutamate and for cysteine and the first enzyme for cysteine biosynthesis.
SO JOURNAL OF BIOLOGICAL CHEMISTRY, (1994 Mar 11) 269 (10) 7473-82.
Journal code: HIV; 2985121R. ISSN: 0021-9258.

L26 ANSWER 18 OF 36 MEDLINE
TI Genomic scanning for expressed sequences in Xp21 identifies the glycerol kinase gene.
SO NATURE GENETICS, (1993 Aug) 4 (4) 367-72.
Journal code: BRO; 9216904. ISSN: 1061-4036.

- L26 ANSWER 19 OF 36 MEDLINE
 TI Lysine 106 of the putative catalytic ATP-binding site of the *Bacillus subtilis* SecA protein is required for **functional complementation** of *Escherichia coli* secA mutants in vivo.
 SO JOURNAL OF BIOLOGICAL CHEMISTRY, (1993 Feb 25) 268 (6) 4504-10.
 Journal code: HIV; 2985121R. ISSN: 0021-9258.
- L26 ANSWER 20 OF 36 MEDLINE
 TI Glutamyl-tRNA reductase from *Escherichia coli* and *Synechocystis* 6803. Gene structure and expression.
 SO JOURNAL OF BIOLOGICAL CHEMISTRY, (1992 Apr 25) 267 (12) 8275-80.
 Journal code: HIV; 2985121R. ISSN: 0021-9258.
- L26 ANSWER 21 OF 36 MEDLINE
 TI Cyclohexadienyl dehydratase from *Pseudomonas aeruginosa*. Molecular cloning of the gene and characterization of the gene product.
 SO JOURNAL OF BIOLOGICAL CHEMISTRY, (1992 Feb 5) 267 (4) 2487-93.
 Journal code: HIV; 2985121R. ISSN: 0021-9258.
- L26 ANSWER 22 OF 36 MEDLINE
 TI Molecular cloning and sequencing of a gene from *alkaliphilic Bacillus firmus* OF4 that **functionally complements** an *Escherichia coli* strain carrying a deletion in the nhaA Na⁺/H⁺ antiporter gene.
 SO JOURNAL OF BIOLOGICAL CHEMISTRY, (1991 Dec 5) 266 (34) 23483-9.
 Journal code: HIV; 2985121R. ISSN: 0021-9258.
- L26 ANSWER 23 OF 36 MEDLINE
 TI De novo purine nucleotide biosynthesis: cloning, sequencing and expression of a chicken PurH cDNA encoding 5-aminoimidazole-4-carboxamide-ribonucleotide transformylase-IMP cyclohydrolase.
 SO GENE, (1991 Oct 15) 106 (2) 197-205.
 Journal code: FOP; 7706761. ISSN: 0378-1119.
- L26 ANSWER 24 OF 36 MEDLINE
 TI Cloning and expression of avian glutamine phosphoribosylpyrophosphate amidotransferase. Conservation of a bacterial propeptide sequence supports a role for posttranslational processing.
 SO JOURNAL OF BIOLOGICAL CHEMISTRY, (1990 Dec 5) 265 (34) 21152-9.
 Journal code: HIV; 2985121R. ISSN: 0021-9258.
- L26 ANSWER 25 OF 36 MEDLINE
 TI Cloning of a cDNA encoding adenylosuccinate lyase by **functional complementation** in *Escherichia coli*.
 SO JOURNAL OF BIOLOGICAL CHEMISTRY, (1990 Jun 5) 265 (16) 9011-4.
 Journal code: HIV; 2985121R. ISSN: 0021-9258.
- L26 ANSWER 26 OF 36 MEDLINE
 TI Complementation and genetic inactivation: two alternative mechanisms leading to prototrophy in diploid bacterial clones.
 SO MOLECULAR AND GENERAL GENETICS, (1984) 196 (3) 488-93.
 Journal code: NGP; 0125036. ISSN: 0026-8925.
- L26 ANSWER 27 OF 36 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
 TI Conserved amino acids in the N- and C-terminal domains of integral membrane transporter FhuB define sites important for intra- and intermolecular interactions.
 SO Molecular Microbiology, (1996) Vol. 20, No. 1, pp. 223-232. ISSN: 0950-382X.
- L26 ANSWER 28 OF 36 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
 TI A *Lactococcus lactis* gene encodes a membrane protein with putative ATPase activity that is homologous to the essential *Escherichia coli* ftsH gene product.
 SO Microbiology (Reading), (1994) Vol. 140, No. 10, pp. 2601-2610. ISSN: 1350-0872.
- L26 ANSWER 29 OF 36 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
 TI Isolation and characterization of the secE homologue gene of *Bacillus subtilis*.
 SO Molecular Microbiology, (1993) Vol. 10, No. 1, pp. 133-142. ISSN: 0950-382X.
- L26 ANSWER 30 OF 36 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
 TI Environmental regulation of the fim switch controlling type 1 fimbrial phase variation in *Escherichia coli* K-12: Effects of temperature and media.
 SO Journal of Bacteriology, (1993) Vol. 175, No. 19, pp. 6186-6193. ISSN: 0021-9193.
- L26 ANSWER 31 OF 36 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
 TI Isolation and characterization of *Bacillus subtilis* genes involved in siderophore biosynthesis: Relationship between *Bacillus subtilis* sfp-0 and *Escherichia coli* entD genes.
 SO Journal of Bacteriology, (1993) Vol. 175, No. 19, pp. 6203-6211. ISSN: 0021-9193.
- L26 ANSWER 32 OF 36 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
 TI The aroQ-encoded monofunctional chorismate mutase (CM-F) protein is a periplasmic enzyme in *Erwinia herbicola*.
 SO Journal of Bacteriology, (1993) Vol. 175, No. 15, pp. 4729-4737. ISSN: 0021-9193.
- L26 ANSWER 33 OF 36 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
 TI DE-NOVO PURINE NUCLEOTIDE BIOSYNTHESIS CLONING OF A COMPLEMENTARY DNA ENCODING ADENYLOSUCCINATE LYASE BY **FUNCTIONAL COMPLEMENTATION** IN *ESCHERICHIA-COLI*.
 SO JOINT MEETING OF THE AMERICAN SOCIETY FOR BIOCHEMISTRY AND MOLECULAR BIOLOGY, AND THE AMERICAN ASSOCIATION OF IMMUNOLOGISTS, NEW ORLEANS, LOUISIANA, USA, JUNE 4-7, 1990. FASEB (FED AM SOC EXP BIOL) J. (1990) 4 (7), A1986. CODEN: FAJOEC. ISSN: 0892-6638.
- L26 ANSWER 34 OF 36 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
 TI GENETIC STUDIES ON TEMPERATURE SENSITIVE **MUTANTS OF BACILLUS-SUBTILIS BACTERIO PHAGE SPP-1**.
 SO FOLIA MICROBIOL, (1975) 20 (5), 389-395. CODEN: FOMIAZ. ISSN: 0015-5632.
- L26 ANSWER 35 OF 36 CAPLUS COPYRIGHT 2002 ACS
 TI The *Bacillus subtilis* addAB genes are fully functional in *Escherichia coli*
 SO Mol. Microbiol. (1993), 7(6), 915-23
 CODEN: MOMIEE; ISSN: 0950-382X

L26 ANSWER 36 OF 36 CAPLUS COPYRIGHT 2002 ACS
TI Escherichia coli 4.5S RNA gene function can be complemented by
heterologous bacterial RNA genes
SO J. Bacteriol. (1990), 172(3), 1284-8
CODEN: JOBAAY; ISSN: 0021-9193

=> D HIS

(FILE 'HOME' ENTERED AT 12:48:41 ON 24 MAY 2002)

FILE 'REGISTRY' ENTERED AT 12:49:49 ON 24 MAY 2002

E "SPOIIIIE"/CN 25

L1 1 S E4

E "SPOOJ"/CN 25

L2 1 S E4

INDEX 'ADISALERTS, ADISINSIGHT, ADISNEWS,
AGRICOLA, ANABSTR, AQUASCI,
BIOBUSINESS, BIOCOMMERCE, BIOSIS, BIOTECHABS,
BIOTECHDS, BIOTECHNO, CABA,
CANCERLIT, CAPLUS, CEABA-VTB, CEN, CIN, CONFSCI,
CROPB, CROPU, DDFB,
DDFU, DGENE, DRUGB, DRUGLAUNCH, DRUGMONOG2, ...'
ENTERED AT 12:53:52 ON
24 MAY 2002

SEA SPOIIIIE

1 FILE AQUASCI
47 FILE BIOSIS
6 FILE BIOTECHABS
6 FILE BIOTECHDS
28 FILE BIOTECHNO
1 FILE CABA
50 FILE CAPLUS
1 FILE CEABA-VTB
1 FILE CONFSCI
6 FILE DGENE
30 FILE EMBASE
23 FILE ESBIODASE
3 FILE FSTA
54 FILE GENBANK
8 FILE IFIPAT
5 FILE JICST-EPLUS
34 FILE LIFESCI
37 FILE MEDLINE
9 FILE PASCAL
2 FILE PROMT
34 FILE SCISEARCH
8 FILE TOXCENTER
17 FILE USPATFULL
5 FILE WPIDS
5 FILE WPINDEX
L3 QUE SPOIIIIE

SEA SPOOJ

27 FILE BIOSIS
4 FILE BIOTECHABS
4 FILE BIOTECHDS
16 FILE BIOTECHNO
1 FILE CABA
19 FILE CAPLUS
15 FILE EMBASE
10 FILE ESBIODASE
1 FILE FEDRIP
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11 FILE GENBANK
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1 FILE JICST-EPLUS
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10 FILE MEDLINE
2 FILE PASCAL

13 FILE SCISEARCH
8 FILE TOXCENTER
9 FILE USPATFULL
2 FILE WPIDS
2 FILE WPINDEX
L4 QUE SPOOJ

FILE 'BIOSIS, CAPLUS' ENTERED AT 12:55:42 ON 24 MAY 2002

L5 97 S SPOIIIIE

L6 46 S SPOOJ

L7 3 S L5 AND L6

L8 3 DUP REM L7 (0 DUPLICATES REMOVED)

FILE 'MEDLINE, CAPLUS, BIOSIS' ENTERED AT 13:26:26 ON 24 MAY 2002

L9 45878 S REPORTER GENE

L10 317475 S COMPLEMENTA?

L11 2166 S L9 AND L10

L12 822 S L9(P)L10

L13 6401 S SIGMA FACTOR

L14 2900 S SIGMA F

L15 0 S L12 AND L14

L16 400 DUP REM L12 (422 DUPLICATES REMOVED)

FILE 'REGISTRY' ENTERED AT 13:31:57 ON 24 MAY 2002

E "PROKARYOTE"/CN 25

E "BACTERIUM"/CN 25

FILE 'MEDLINE, BIOSIS, CAPLUS' ENTERED AT 13:33:15 ON 24 MAY 2002

L17 400 S L16

L18 70987 S SUBTILIS

L19 4 S L17 AND L18

L20 556256 S COMPLEMENT?

L21 3739694 S FUNCTION?

L22 0 S L20(W)L21

L23 4121 S L20(A)L21

L24 106 S L18 AND L23

L25 46 DUP REM L24 (60 DUPLICATES REMOVED)

L26 36 S L25 NOT PY>1998

=> S L9 AND L23

L27 38 L9 AND L23

=> DUP REM L27

PROCESSING COMPLETED FOR L27

L28 17 DUP REM L27 (21 DUPLICATES REMOVED)

=> D TI SO 1-17

L28 ANSWER 1 OF 17 CAPLUS COPYRIGHT 2002 ACS

TI Escherichia coli adenylate cyclase deficient strain for bacterial
two-hybrid system based on a cAMP signaling cascade
SO PCT Int. Appl., 45 pp.

CODEN: PIXXD2

L28 ANSWER 2 OF 17 MEDLINE

DUPLICATE 1

TI Multiple domains are required for the toxic activity of Pseudomonas
aeruginosa ExoU.

SO JOURNAL OF BACTERIOLOGY, (2001 Jul) 183 (14) 4330-44.

Journal code: HH3; 2985120R. ISSN: 0021-9193.

L28 ANSWER 3 OF 17 BIOSIS COPYRIGHT 2002 BIOLOGICAL
ABSTRACTS INC.

TI Transient transfection of polarized epithelial monolayers with CFTR
and

reporter genes using lipid transfecting reagents.

SO FASEB Journal, (March 8, 2001) Vol. 15, No. 5, pp. A848. print.

Meeting Info.: Annual Meeting of the Federation of American
Societies for

Experimental Biology on Experimental Biology 2001 Orlando,
Florida, USA

March 31-April 04, 2001
ISSN: 0892-6638.

L28 ANSWER 4 OF 17 CAPLUS COPYRIGHT 2002 ACS
TI Functional Analysis of the Influenza A Virus cRNA Promoter and
Construction of an Ambisense Transcription System
SO Virology (2001), 289(2), 400-410
CODEN: VIRLAX; ISSN: 0042-6822

L28 ANSWER 5 OF 17 BIOSIS COPYRIGHT 2002 BIOLOGICAL
ABSTRACTS INC.
TI Regulator of G-protein signaling z1 (RGSz1) interacts with Galphai
subunit
and regulates Galphai mediated signal transduction.
SO Society for Neuroscience Abstracts, (2001) Vol. 27, No. 1, pp. 108.
print.
Meeting Info.: 31st Annual Meeting of the Society for Neuroscience
San
Diego, California, USA November 10-15, 2001
ISSN: 0190-5295.

L28 ANSWER 6 OF 17 MEDLINE DUPLICATE 2
TI Regulation of tomato leaf curl viral gene expression in host tissues.
SO MOLECULAR PLANT-MICROBE INTERACTIONS, (2000
May) 13 (5) 529-37.
Journal code: A9P; 9107902. ISSN: 0894-0282.

L28 ANSWER 7 OF 17 MEDLINE DUPLICATE 3
TI General or cell type-specific deletion and replacement of connexin-
coding
DNA in the mouse.
SO METHODS, (2000 Feb) 20 (2) 205-18.
Journal code: CPO; 9426302. ISSN: 1046-2023.

L28 ANSWER 8 OF 17 CAPLUS COPYRIGHT 2002 ACS
TI A bacterial multi-hybrid system and applications
SO PCT Int. Appl., 66 pp.
CODEN: PIXXD2

L28 ANSWER 9 OF 17 MEDLINE DUPLICATE 4
TI Characterization of baculovirus repeated open reading frames (bro)
in
Bombyx mori nucleopolyhedrovirus.
SO JOURNAL OF VIROLOGY, (1999 Dec) 73 (12) 10339-45.
Journal code: KCV; 0113724. ISSN: 0022-538X.

L28 ANSWER 10 OF 17 MEDLINE DUPLICATE 5
TI Iron regulation and pathogenicity in Erwinia chrysanthemi 3937:
role of
the Fur repressor protein.
SO MOLECULAR PLANT-MICROBE INTERACTIONS, (1999 Feb)
12 (2) 119-28.
Journal code: A9P; 9107902. ISSN: 0894-0282.

L28 ANSWER 11 OF 17 MEDLINE DUPLICATE 6
TI The products of the yeast MMS2 and two human homologs
(hMMS2 and CROC-1)
define a structurally and functionally conserved Ubc-like protein
family.
SO NUCLEIC ACIDS RESEARCH, (1998 Sep 1) 26 (17) 3908-14.
Journal code: O8L; 0411011. ISSN: 0305-1048.

L28 ANSWER 12 OF 17 MEDLINE DUPLICATE 7
TI Identification of a negative regulator of gibberellin action, HvSPY,
in
barley.
SO PLANT CELL, (1998 Jun) 10 (6) 995-1007.
Journal code: BJU; 9208688. ISSN: 1040-4651.

L28 ANSWER 13 OF 17 MEDLINE DUPLICATE 8
TI Mms4, a putative transcriptional (co)activator, protects
Saccharomyces
cerevisiae cells from endogenous and environmental DNA damage.
SO MOLECULAR AND GENERAL GENETICS, (1998 Apr) 257 (6)

614-23.
Journal code: NGP; 0125036. ISSN: 0026-8925.

L28 ANSWER 14 OF 17 CAPLUS COPYRIGHT 2002 ACS
TI A stable shuttle vector system for efficient genetic complementation
of
Helicobacter pylori strains by transformation and conjugation
SO Molecular & General Genetics (1998), 257(5), 519-528
CODEN: MGGEAE; ISSN: 0026-8925

L28 ANSWER 15 OF 17 MEDLINE DUPLICATE 9
TI Influence of gene dosage and autoregulation of the regulatory genes
INO2
and INO4 on inositol/choline-repressible gene transcription in the
yeast
Saccharomyces cerevisiae.
SO CURRENT GENETICS, (1997 Jun) 31 (6) 462-8.
Journal code: CUG; 8004904. ISSN: 0172-8083.

L28 ANSWER 16 OF 17 MEDLINE DUPLICATE 10
TI Iron-responsive genetic regulation in Campylobacter jejuni: cloning
and
characterization of a fur homolog.
SO JOURNAL OF BACTERIOLOGY, (1994 Sep) 176 (18) 5852-6.
Journal code: HH3; 2985120R. ISSN: 0021-9193.

L28 ANSWER 17 OF 17 MEDLINE DUPLICATE 11
TI Expression of yeast cytochrome c1 is controlled at the
transcriptional
level by glucose, oxygen and haem.
SO MOLECULAR AND GENERAL GENETICS, (1992 Apr) 232 (3)
447-59.
Journal code: NGP; 0125036. ISSN: 0026-8925.

=> D IBIB AB 16,14,13,11

L28 ANSWER 16 OF 17 MEDLINE DUPLICATE 10
ACCESSION NUMBER: 94364968 MEDLINE
DOCUMENT NUMBER: 94364968 PubMed ID: 8083178
TITLE: Iron-responsive genetic regulation in Campylobacter
jejuni:
cloning and characterization of a fur homolog.
AUTHOR: Wooldridge K G; Williams P H; Ketley J M
CORPORATE SOURCE: Department of Genetics, University of
Leicester, England.
SOURCE: JOURNAL OF BACTERIOLOGY, (1994 Sep) 176
(18) 5852-6.
Journal code: HH3; 2985120R. ISSN: 0021-9193.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-X78965
ENTRY MONTH: 199410
ENTRY DATE: Entered STN: 19941021
Last Updated on STN: 19980206
Entered Medline: 19941012

AB The Fur protein of Escherichia coli represses transcription from
Fur-responsive genes in an iron-dependent manner. We have
demonstrated a
Fur-like iron-responsive genetic regulatory activity operating in
Campylobacter jejuni by using a chloramphenicol acetyl transferase
reporter gene separated from its promoter by a synthetic
Fur-responsive operator. A fur-like gene has been cloned from C.
jejuni by
partial functional complementation of an E. coli fur
mutation. Sequence analysis has shown that, at the amino acid level,
the
C. jejuni Fur protein is 35% identical with its E. coli counterpart.

L28 ANSWER 14 OF 17 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1998:297690 CAPLUS
DOCUMENT NUMBER: 129:63700

TITLE: A stable shuttle vector system for efficient genetic complementation of *Helicobacter pylori* strains by transformation and conjugation

AUTHOR(S): Heuermann, D.; Haas, R.

CORPORATE SOURCE: Max-Planck-Institut für Biologie, Abteilung Infektionsbiologie, Tübingen, D-72076, Germany

SOURCE: Molecular & General Genetics (1998), 257(5), 519-528

CODEN: MGGEAE; **ISSN:** 0026-8925

PUBLISHER: Springer-Verlag

DOCUMENT TYPE: Journal

LANGUAGE: English

AB A versatile plasmid shuttle vector system was constructed, which is useful for genetic complementation of *Helicobacter pylori* strains or mutants with cloned genes of homologous or heterologous origin. The individual plasmid vectors consist of the minimal essential genetic elements, including an origin of replication for *Escherichia coli*, a *H. pylori*-specific replicon originally identified on a small cryptic *H. pylori* plasmid, an *oriT* sequence and a multiple cloning site. Shuttle plasmid pHe12 carries a chloramphenicol resistance cassette (*catGC*) and pHe13 contains a kanamycin resistance gene (*aphA-3*) as the selectable marker; both are functional in *E. coli* and *H. pylori*. The shuttle plasmids were introduced into the *H. pylori* strain P1 by natural transformation. A efficiency of 7.0 .times. 10⁻⁷ and 4.7 .times. 10⁻⁷ transformants per viable recipient was achieved with pHe12 and pHe13, resp., and both vectors showed stable, autonomous replication in *H. pylori*. An approx. 100-fold higher *H. pylori* transformation rate was obtained when the shuttle vectors for transformation were isolated from the homologous *H. pylori* strain, rather than *E. coli*, indicating that DNA restriction and modification mechanisms play a crucial role in plasmid transformation. Interestingly, both shuttle vectors could also be mobilized efficiently from *E. coli* into different *H. pylori* recipients, with pHe12 showing an efficiency of 2.0 .times. 10⁻⁵ transconjugants per viable *H. pylori* P1 recipient. Thus, DNA restriction seems to be strongly reduced or absent during conjugal transfer. The functional complementation of a *recA*-deficient *H. pylori* mutant by the cloned *H. pylori* *recA*⁺ gene, and the expression of the heterologous green fluorescent protein (GFP) in *H. pylori* demonstrate the general usefulness of this system, which will significantly facilitate the mol. anal. of *H. pylori* virulence factors in the future.

L28 ANSWER 13 OF 17 MEDLINE DUPLICATE 8

ACCESSION NUMBER: 1998265920 **MEDLINE**

DOCUMENT NUMBER: 98265920 **PubMed ID:** 9604884

TITLE: Mms4, a putative transcriptional (co)activator, protects *Saccharomyces cerevisiae* cells from endogenous and environmental DNA damage.

AUTHOR: Xiao W; Chow B L; Milo C N

CORPORATE SOURCE: Department of Microbiology, University of Saskatchewan, Saskatoon, Canada.. xiaow@sask.usask.ca

SOURCE: MOLECULAR AND GENERAL GENETICS, (1998 Apr) 257 (6) 614-23.

Journal code: NGP; 0125036. **ISSN:** 0026-8925.

PUB. COUNTRY: GERMANY: Germany, Federal Republic of

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 199806

ENTRY DATE: Entered STN: 19980618

Last Updated on STN: 19980618

Entered Medline: 19980611

AB mms4-1 is one of several *Saccharomyces cerevisiae* mutants that exhibit an increased sensitivity to methyl methanesulfonate (MMS), but not to UV or X-rays. We have isolated the MMS4 gene by functional complementation of the MMS-sensitive phenotype in the mms4-1 strain. The MMS4 gene encodes a 691-amino acid, 78.7-kDa protein. The deduced Mms4 protein does not show significant homology to any of the known proteins in the database. However, several putative functional domains suggest that it may be a nuclear protein capable of interacting with other proteins. Examination of the mms4delta mutant phenotype indicates that the mutation not only sensitizes DNA to methylating and ethylating agents, but also to other DNA damage that blocks DNA replication. However, the mms4delta mutant appears to be more sensitive to chronic treatment than to acute treatment by DNA-damaging agents. Furthermore, the spontaneous mutation rate increases significantly in the mms4delta mutant. Mms4 alone, when fused to a Gal4 DNA-binding domain, is able to activate P(GAL1)-lacZ and P(GAL1)-HIS3 reporter genes in a two-hybrid system; the Mms4 transactivation domain maps to the highly acidic N-terminal region. These results collectively suggest that Mms4 may function as a transcriptional (co)activator and play an important role in DNA repair and/or synthesis.

L28 ANSWER 11 OF 17 MEDLINE DUPLICATE 6

ACCESSION NUMBER: 1998371225 **MEDLINE**

DOCUMENT NUMBER: 98371225 **PubMed ID:** 9705497

TITLE: The products of the yeast MMS2 and two human homologs (hMMS2 and CROC-1) define a structurally and functionally conserved Ubc-like protein family.

AUTHOR: Xiao W; Lin S L; Broomfield S; Chow B L; Wei Y F

CORPORATE SOURCE: Department of Microbiology, University of Saskatchewan, Saskatoon, SK S7N 5E5, Canada.. xiaow@sask.usask.ca

SOURCE: NUCLEIC ACIDS RESEARCH, (1998 Sep 1) 26 (17) 3908-14.

Journal code: O8L; 0411011. **ISSN:** 0305-1048.

PUB. COUNTRY: ENGLAND: United Kingdom

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

OTHER SOURCE: GENBANK-AF049140

ENTRY MONTH: 199810

ENTRY DATE: Entered STN: 19981021

Last Updated on STN: 19981021

Entered Medline: 19981015

AB Eukaryotic genes encoding ubiquitin-conjugating enzyme (Ubc)-like proteins have been isolated from both human and yeast cells. The CROC-1 gene was isolated by its ability to transactivate c- fos expression in cell culture through a tandem repeat enhancer sequence. The yeast MMS2 gene was cloned by its ability to complement the methyl methanesulfonate sensitivity of the mms2-1 mutant and was later shown to be involved in DNA post-replication repair. We report here the identification of a human MMS2 (hMMS2) cDNA encoding a novel human Ubc-like protein.

hMMS2 and CROC-1

share >90% amino acid sequence identity, but their DNA probes hybridize to distinct transcripts. hMMS2 and CROC-1 also share approximately 50% identity and 75% similarity with the entire length of yeast Mms2. Unlike CROC-1, whose transcript appears to be elevated in all tumor cell lines examined, the hMMS2 transcript is only elevated in some tumor cell lines. Collectively, these results indicate that eukaryotic cells may contain a highly conserved family of Ubc-like proteins that play roles in diverse cellular processes, ranging from DNA repair to signal transduction and cell differentiation. The hMMS2 and CROC-1 genes are able to functionally complement the yeast mms2 defects with regard to sensitivity to DNA damaging agents and spontaneous mutagenesis. Conversely, both MMS2 and hMMS2 were able to transactivate a c-fos - CAT reporter gene in Rat-1 cells in a transient co-transfection assay. We propose that either these proteins function in a common cellular process, such as DNA repair, or they exert their diverse biological roles through a similar biochemical interaction relative to ubiquitination.

=> D IBIB AB L26

36,35,33,31,29,28,26,25,22,21,19,16,13,12,11,9,6,5,3

L26 ANSWER 36 OF 36 CAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 1990:152712 CAPLUS

DOCUMENT NUMBER: 112:152712

TITLE: Escherichia coli 4.5S RNA gene function can be complemented by heterologous bacterial RNA genes

AUTHOR(S): Struck, Joachim C. R.; Lempicki, Richard A.; Toschka,

Holger Y.; Erdmann, Volker A.; Fournier, Maurille J.
CORPORATE SOURCE: Inst. Biochem., Freie Univ. Berlin, Berlin, D-1000,

Fed. Rep. Ger.

SOURCE: J. Bacteriol. (1990), 172(3), 1284-8

CODEN: JOBAAY; ISSN: 0021-9193

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The essential 4.5 S RNA gene of E. coli can be complemented by 4.5 S

RNA-like genes from 3 other eubacteria, including both gram-pos. and

gram-neg. organisms. Two of the genes encode RNAs similar in size to the

E. coli species; the third, from Bacillus subtilis, specifies an RNA more than twice as large. The heterologous genes are

expressed efficiently in E. coli, and the product RNAs resemble those produced by

cognate cells. It is concluded that the heterologous RNAs can replace E.

coli 4.5 S RNA and that the essential function of 4.5 S RNA is evolutionarily conserved. A consensus structure is presented for the functionally-related 4.5 S RNA homologs.

L26 ANSWER 35 OF 36 CAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 1993:248685 CAPLUS

DOCUMENT NUMBER: 118:248685

TITLE: The Bacillus subtilis addAB genes are fully functional in Escherichia coli

AUTHOR(S): Kooistra, Jan; Haijema, Bert Jan; Venema, Gerard

CORPORATE SOURCE: Dep. Genet., Univ. Groningen, Haren,

9751 NN, Neth.

SOURCE: Mol. Microbiol. (1993), 7(6), 915-23

CODEN: MOMIEE; ISSN: 0950-382X

DOCUMENT TYPE: Journal

LANGUAGE: English

AB An E. coli recBCD deletion mutant was transformed with plasmids contg. the

B. subtilis add genes. The transformants had relatively high ATP-dependent exonuclease and ATP-dependent helicase activities, and their

viability, the ability to repair UV-damaged DNA, and the recombination in

conjugation were nearly completely restored. The B. subtilis Add enzyme did not show Chi-activity in phage lambda.

recombination. The

individual B. subtilis Add proteins were not able to form an enzymically active complex with the E. coli RecBCD proteins, and they

could not complement the recBCD deficiency. Evidence is presented that

only 2 subunits are involved in the B. subtilis ATP-dependent exonuclease. This is in contrast to E. coli in which the RecBCD enzyme

consists of three subunits.

L26 ANSWER 33 OF 36 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 1990:346193 BIOSIS

DOCUMENT NUMBER: BR39:41454

TITLE: DE-NOVO PURINE NUCLEOTIDE BIOSYNTHESIS CLONING OF A

COMPLEMENTARY DNA ENCODING

ADENYLOSUCCINATE LYASE BY

FUNCTIONAL COMPLEMENTATION IN ESCHERICHIA-COLI.

AUTHOR(S): BADLAK J; AIMI J; WILLIAMS J; CHEN Z; ZALKIN H; DIXON J E

CORPORATE SOURCE: PURDUE UNIV., DEP. OF BIOCHEM., WEST LAFAYETTE, INDIANA 47907.

SOURCE: JOINT MEETING OF THE AMERICAN SOCIETY FOR BIOCHEMISTRY AND

MOLECULAR BIOLOGY, AND THE AMERICAN ASSOCIATION OF

IMMUNOLOGISTS, NEW ORLEANS, LOUISIANA, USA, JUNE 4-7, 1990.

FASEB (FED AM SOC EXP BIOL) J, (1990) 4 (7), A1986. CODEN: FAJOEC. ISSN: 0892-6638.

DOCUMENT TYPE: Conference

FILE SEGMENT: BR; OLD

LANGUAGE: English

L26 ANSWER 31 OF 36 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 1993:499267 BIOSIS

DOCUMENT NUMBER: PREV199396123274

TITLE: Isolation and characterization of Bacillus subtilis genes involved in siderophore biosynthesis: Relationship between Bacillus subtilis sfp-0 and Escherichia coli entD genes.

AUTHOR(S): Grossman, Trudy H.; Tuckman, Margareta; Ellestad, Sarah;

Osburne, Marcia S. (1)

CORPORATE SOURCE: (1) Procept Inc., 840 Memorial Dr., Cambridge, MA 02139 USA

SOURCE: Journal of Bacteriology, (1993) Vol. 175, No. 19; pp. 6203-6211.

ISSN: 0021-9193.

DOCUMENT TYPE: Article

LANGUAGE: English

AB In response to iron deprivation, Bacillus subtilis secretes a catecholic siderophore, 2,3-dihydroxybenzoyl glycine, which is similar to

the precursor of the Escherichia coli siderophore enterobactin. We

isolated two sets of *B. subtilis* DNA sequences that complemented the mutations of several *E. coli* siderophore-deficient (ent) mutants with defective enterobactin biosynthesis enzymes. One set contained DNA sequences that complemented only an entD mutation. The second set contained DNA sequences that complemented various combinations of entB, entE, entC, and entA mutations. The two sets of DNA sequences did not appear to overlap. A *B. subtilis* mutant containing an insertion in the region of the entD homolog grew much more poorly in low-iron medium and with markedly different kinetics. These data indicate that (i) at least five of the siderophore biosynthesis genes of *B. subtilis* can function in *E. coli*, (ii) the genetic organization of these siderophore genes in *B. subtilis* is similar to that in *E. coli*, and (iii) the *B. subtilis* entD homolog is required for efficient growth in low-iron medium. The nucleotide sequence of the *B. subtilis* DNA contained in plasmid pENTA22, a clone expressing the *B. subtilis* entD homolog, revealed the presence of at least two genes. One gene was identified as *sfp-0*, a previously reported gene involved in the production of surfactin in *B. subtilis* and which is highly homologous to the *E. coli* entD gene. We present evidence that the *E. coli* entD and *B. subtilis* *sfp-0* genes are interchangeable and that their products are members of a new family of proteins which function in the secretion of peptide molecules.

L26 ANSWER 29 OF 36 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 1993:585144 BIOSIS

DOCUMENT NUMBER: PREV199497004514

TITLE: Isolation and characterization of the secE homologue gene of *Bacillus subtilis*.

AUTHOR(S): Jeong, Sang Min; Yoshikawa, Hirofumi; Takahashi, Hideo (1)

CORPORATE SOURCE: (1) Inst. Molecular Cellular Biosciences, Univ. Tokyo,

Bunkyo-ku, Tokyo 113 Japan

SOURCE: Molecular Microbiology, (1993) Vol. 10, No. 1, pp. 133-142.

ISSN: 0950-382X.

DOCUMENT TYPE: Article

LANGUAGE: English

AB A 4.0 kb EcoRI fragment of *Bacillus subtilis* conferring thiostrepton resistance was cloned and characterized. By nucleotide sequencing of the relevant region, six open reading frames were established, which corresponded to a part of *spoOH*, a ribosomal protein

gene (*rpmG*), an unidentified open reading frame (*orfE*), a transcription

antiterminator gene *nusG*, and ribosomal protein genes *rplK* and *rplA*. The

orfE-encoded 59-amino-acid polypeptide had a low, but significant, sequence similarity with the carboxy-terminal region of the *Escherichia*

coli SecE protein. A cold-sensitive *secE* mutation of *E. coli* was complemented by the plasmid-borne *orfE* sequence. Furthermore, the normal

processing of a proOmpA protein was observed when the *secE* cold-sensitive

strain carried an *orfE* plasmid, indicating that *orfE* is the *secE* homologue

of *B. subtilis*. The *B. subtilis* *secE* has only one transmembrane sequence compared to the three in *E. coli*.

L26 ANSWER 28 OF 36 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 1994:545332 BIOSIS

DOCUMENT NUMBER: PREV199598004880

TITLE: A *Lactococcus lactis* gene encodes a membrane protein with

putative ATPase activity that is homologous to the essential *Escherichia coli* *ftsH* gene product.

AUTHOR(S): Nilsson, Dan (1); Lauridsen, Anette A.; Tomoyasu, Toshifumi; Ogura, Teru

CORPORATE SOURCE: (1) Dep. Genetics, Chr. Hansen's Lab. Danmark A/S, Boge

Alle 10-12, DK-2970 Horsholm Denmark

SOURCE: Microbiology (Reading), (1994) Vol. 140, No. 10, pp. 2601-2610.

ISSN: 1350-0872.

DOCUMENT TYPE: Article

LANGUAGE: English

AB A gene, encoding a protein homologous to an essential *Escherichia coli*

protein, FtsH, was identified adjacent to the *hpt* gene and the *trnA* operon

in the Gram-positive bacterium *Lactococcus lactis*. The deduced amino acid

sequence of the gene product showed full-length similarity to FtsH of *E.*

coli, *Yme1p* of *Saccharomyces cerevisiae* and a conserved region found in a

new family of putative ATPases. In-frame fusions of *L. lactis* *ftsH* and

phoA1 in *E. coli*, and immunodetection of the *L. lactis* FtsH protein in

cell fractions using anti-*E. coli* FtsH serum showed that *L. lactis* *ftsH* was expressed and encodes a membrane protein. When contained on

a high copy number plasmid, the *L. lactis* *ftsH* gene complemented the lethality of

a DELTA-*ftsH3::kan* mutation in *E. coli* at 37 degree C and below, indicating that the *L. lactis* *ftsH* gene can functionally replace the *E. coli* *ftsH* gene to some extent. The resulting *E. coli* strain showed temperature sensitivity and salt sensitivity. A *L. lactis* mutant with an insertion into *ftsH* was salt-, heat- and cold-sensitive. These results suggest that FtsH is somehow involved in stress responses. Southern hybridization analysis indicated that genes homologous to *ftsH* of *L. lactis* were also present in *Bacillus subtilis*, and several *Lactobacillus* and *Leuconostoc* species, suggesting high conservation of *ftsH* in bacterial species.

L26 ANSWER 26 OF 36 MEDLINE

ACCESSION NUMBER: 85060517 MEDLINE

DOCUMENT NUMBER: 85060517 PubMed ID: 6438446

TITLE: Complementation and genetic inactivation: two alternative

mechanisms leading to prototrophy in diploid bacterial clones.

AUTHOR: Levi-Meyrueis C; Sanchez-Rivas C

SOURCE: MOLECULAR AND GENERAL GENETICS, (1984) 196 (3) 488-93.

Journal code: NGP; 0125036. ISSN: 0026-8925.

PUB. COUNTRY: GERMANY, WEST: Germany, Federal Republic of

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 198501

ENTRY DATE: Entered STN: 19900320

Last Updated on STN: 19900320

Entered Medline: 19850110

AB Evidence for diploidy at loci located all around the *Bacillus subtilis* chromosome previously led us to refer to the prototrophic bacterial clones produced by fusion of polyauxotrophic protoplasts as complementing diploid clones (Levi-Meyrueis et al. 1980; Sanchez-Rivas

1982). In this paper, evidence is presented that gene inactivation may occur in such clones, as judged from the unequal expression of three unselected markers and their low transforming activity in cell lysates, an

established property of inactivated genes (Bohin et al. 1982). The insensitivity to protease treatment of the lysates and also the low

transforming activity observed with purified DNA may indicate that chromosome inactivation does not necessarily result from the mere attachment of proteins to DNA. Cotransfer by transformation of similarly expressed genes, initially located on separate chromosomes, suggests that genetic recombination has taken place, resulting in the reassortment of active and inactive genes on separate chromosomes. Several genetic structures compatible with the observations are presented which illustrate that prototrophy may result from such reassortment as well as from **functional complementation**.

L26 ANSWER 25 OF 36 MEDLINE
 ACCESSION NUMBER: 90264380 MEDLINE
 DOCUMENT NUMBER: 90264380 PubMed ID: 2111814
 TITLE: Cloning of a cDNA encoding adenylosuccinate lyase by **functional complementation** in *Escherichia coli*.
 AUTHOR: Aimi J; Badylak J; Williams J; Chen Z D; Zalkin H; Dixon J
 E
 CORPORATE SOURCE: Department of Biochemistry, Purdue University, West Lafayette, Indiana 47907.
 CONTRACT NUMBER: 18024 (NIAID)
 AI 27713 (NIGMS)
 GM 24658
 SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (1990 Jun 5) 265 (16) 9011-4.
 Journal code: HIV; 2985121R. ISSN: 0021-9258.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-M37901
 ENTRY MONTH: 199007
 ENTRY DATE: Entered STN: 19900810
 Last Updated on STN: 19900810
 Entered Medline: 19900702
 AB Adenylosuccinate lyase was cloned by **functional complementation** of an *Escherichia coli* purB mutant using an avian liver cDNA expression library. The derived amino acid sequence is homologous to the bacterial purB-encoded adenylosuccinate lyase which catalyzes the same two steps in purine biosynthesis as the enzyme from animals. Avian adenylosuccinate lyase also shows regions of extensive sequence similarity to the urea cycle enzyme, argininosuccinate lyase. This homology suggests a similar mechanism for catalysis. Homology of adenylosuccinate and argininosuccinate lyases is intriguing because chickens do not utilize the urea cycle in nitrogen excretion. This is the first report of the cloning of a eukaryotic cDNA encoding adenylosuccinate lyase, and it affords a route to isolate the corresponding human gene which has been suggested to be defective in autistic children.

L26 ANSWER 22 OF 36 MEDLINE
 ACCESSION NUMBER: 92078231 MEDLINE
 DOCUMENT NUMBER: 92078231 PubMed ID: 1660475
 TITLE: Molecular cloning and sequencing of a gene from alkaliphilic *Bacillus firmus* OF4 that **functionally complements** an *Escherichia coli* strain carrying a deletion in the nhaA Na⁺/H⁺ antiporter gene.
 AUTHOR: Ivey D M; Guffanti A A; Bossewitch J S; Padan E; Krulwich T
 A
 CORPORATE SOURCE: Department of Biochemistry, Mount Sinai

School of Medicine,
 City University of New York, New York.
 SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (1991 Dec 5) 266 (34) 23483-9.
 Journal code: HIV; 2985121R. ISSN: 0021-9258.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-M55199; GENBANK-M55200; GENBANK-M55201; GENBANK-M73530; GENBANK-M96682; GENBANK-S66610; GENBANK-S66768; GENBANK-S69489; GENBANK-S69493; GENBANK-S69544
 ENTRY MONTH: 199201
 ENTRY DATE: Entered STN: 19920202
 Last Updated on STN: 19920202
 Entered Medline: 19920113
 AB A gene has been cloned from a DNA library from alkaliphilic *Bacillus firmus* OF4 that **functionally complements** a mutant strain of *Escherichia coli*, NM81, that carries a deletion for one of that strain's Na⁺/H⁺ antiporter genes (δ nhaA). The cloned alkaliphile gene restored to NM81 the ability to grow at pH 7.5 in the presence of 0.6 M NaCl and on 100 mM Li⁺ in the presence of melibiose, and concomitantly led to an increase in the membrane associated Na⁺/H⁺ antiport activity. The biologically active alkaliphile DNA was identified as an incomplete open reading frame, the sequence of which would encode a hydrophobic protein. The insert was used to isolate clones containing the complete open reading frame, which would be predicted to encode a protein with a molecular weight of 42,960 and multiple membrane spanning regions. When the open reading frame was expressed under the control of the T7 promoter, the gene product was localized in the membrane. Southern analysis indicated no homology between the alkaliphile gene, which we propose to call nhaC, and the nhaA gene of *Escherichia coli*, nor with other genes in digests of DNA from *E. coli*, *Bacillus subtilis*, or *Bacillus alcalophilus*. Although there was also no significant similarity between the deduced protein products of the alkaliphile gene and the nhaA gene of *E. coli*, there was a small region of significant similarity between the deduced alkaliphile gene product and the protein encoded by a human Na⁺/H⁺ antiporter gene (Sardet, C., Franchi, A., and Pouyssegur, J. (1989) *Cell* 56, 271-280).

L26 ANSWER 21 OF 36 MEDLINE
 ACCESSION NUMBER: 92129331 MEDLINE
 DOCUMENT NUMBER: 92129331 PubMed ID: 1733946
 TITLE: Cyclohexadienyl dehydratase from *Pseudomonas aeruginosa*.
 Molecular cloning of the gene and characterization of the gene product.
 AUTHOR: Zhao G S; Xia T H; Fischer R S; Jensen R A
 CORPORATE SOURCE: Department of Microbiology and Cell Science, University of Florida, Gainesville 32611.
 SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (1992

Feb 5) 267 (4)

2487-93.

Journal code: HIV; 2985121R. ISSN: 0021-9258.

PUB. COUNTRY: United States

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

OTHER SOURCE: GENBANK-D10517; GENBANK-D10518;
GENBANK-D10519;

GENBANK-D10520; GENBANK-D12749; GENBANK-
D12750;

GENBANK-D12751; GENBANK-D12752; GENBANK-
D12753;

GENBANK-M74132

ENTRY MONTH: 199203

ENTRY DATE: Entered STN: 19920322

Last Updated on STN: 19920322

Entered Medline: 19920303

AB The gene encoding cyclohexadienyl dehydratase (denoted pheC) was cloned

from *Pseudomonas aeruginosa* by **functional complementation** of a pheA auxotroph of *Escherichia coli*. The gene was highly expressed in *E. coli* due to the use of the high-copy

number vector pUC18. The *P. aeruginosa* cyclohexadienyl dehydratase expressed in

E. coli was purified to electrophoretic homogeneity. The latter enzyme

exhibited identical physical and biochemical properties as those obtained

for cyclohexadienyl dehydratase purified from *P. aeruginosa*. The activity

ratios of prephenate dehydratase to arogenate dehydratase remained constant (about 3.3-fold) throughout purification, thus demonstrating a

single protein having broad substrate specificity. The

cyclohexadienyl dehydratase exhibited K_m values of 0.42 mM for prephenate and 0.22 mM for

L-arogenate, respectively. The pheC gene was 807 base pairs in length, encoding a protein with a calculated molecular mass of 30,480 daltons.

This compares with a molecular mass value of 29.5 kDa determined for the

purified enzyme by sodium dodecyl sulfate-polyacrylamide gel electrophoresis. Since the native molecular mass determined by gel filtration was 72 kDa, the enzyme probably is a homodimer.

Comparison of

the deduced amino acid sequence of pheC from *P. aeruginosa* with those of

the prephenate dehydratases of *Corynebacterium glutamicum*, *Bacillus*

subtilis, *E. coli*, and *Pseudomonas stutzeri* by standard pairwise alignments did not establish obvious homology. However, a more detailed

analysis revealed a conserved motif (containing a threonine residue known to be essential for catalysis) that was shared by all of the dehydratase proteins.

L26 ANSWER 19 OF 36 MEDLINE

ACCESSION NUMBER: 93179466 MEDLINE

DOCUMENT NUMBER: 93179466 PubMed ID: 8440733

TITLE: Lysine 106 of the putative catalytic ATP-binding site of the *Bacillus subtilis* SecA protein is required for functional complementation of *Escherichia coli* secA mutants in vivo.

AUTHOR: Klose M; Schimz K L; van der Wolk J; Driessen A J; Freudl R

CORPORATE SOURCE: Institut für Biotechnologie 1, Forschungszentrum Jülich GmbH, Germany.

SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (1993

Feb 25) 268 (6)

4504-10.

Journal code: HIV; 2985121R. ISSN: 0021-9258.

PUB. COUNTRY: United States

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 199303

ENTRY DATE: Entered STN: 19930416

Last Updated on STN: 19930416

Entered Medline: 19930326

AB The SecA protein is a major component of the cellular machinery that

mediates the translocation of proteins across the *Escherichia coli* plasma

membrane. The secA gene from *Bacillus subtilis* was cloned and expressed in *E. coli* under the control of the lac or trc promoter. The temperature-sensitive growth and secretion defects of various *E. coli*

secA

mutants were complemented by the *B. subtilis* SecA protein, provided the protein was expressed at moderate levels. Under overproduction conditions, no complementation was observed. One of the

main features of the SecA protein is the translocation ATPase activity which, together with the protonmotive force, drives the movement of proteins across the plasma membrane. A putative ATP-binding motif

can be

identified in the SecA protein resembling the consensus Walker A type

motif. Replacement of a lysine residue at position 106, which corresponds

to an invariable amino acid residue, in the consensus motif by asparagine

(K106N) resulted in the loss of the ability of the *B. subtilis* SecA protein to complement the growth and secretion defects of *E. coli*

secA mutants. In addition, the presence of the K106N SecA protein interfered with protein translocation, most likely at an ATP-requiring step. We conclude that lysine 106 is part of the catalytic ATP-binding site of the *B. subtilis* SecA protein, which is required for protein translocation in vivo.

L26 ANSWER 16 OF 36 MEDLINE

ACCESSION NUMBER: 95110050 MEDLINE

DOCUMENT NUMBER: 95110050 PubMed ID: 7811002

TITLE: Cloning and nucleotide sequence of *Pseudomonas aeruginosa*

DNA gyrase gyrA gene from strain PAO1 and quinolone-resistant clinical isolates.

AUTHOR: Kureishi A; Diver J M; Beckthold B; Schollaardt T; Bryan L

E

CORPORATE SOURCE: Department of Microbiology and Infectious Diseases,

University of Calgary, Alberta, Canada.

SOURCE: ANTIMICROBIAL AGENTS AND CHEMOTHERAPY, (1994 Sep) 38 (9)

1944-52.

Journal code: 6HK; 0315061. ISSN: 0066-4804.

PUB. COUNTRY: United States

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

OTHER SOURCE: GENBANK-L29417

ENTRY MONTH: 199501

ENTRY DATE: Entered STN: 19950215

Last Updated on STN: 19950215

Entered Medline: 19950127

AB The *Pseudomonas aeruginosa* DNA gyrase gyrA gene was cloned and sequenced

from strain PAO1. An open reading frame of 2,769 bp was found; it coded

for a protein of 923 amino acids with an estimated molecular mass of 103

kDa. The derived amino acid sequence shared 67% identity with *Escherichia coli* GyrA and 54% identity with *Bacillus subtilis* GyrA, although conserved regions were present throughout the sequences, particularly toward the N terminus. Complementation of an *E. coli* mutant with a temperature-sensitive *gyrA* gene with the PAO1 *gyrA* gene showed that the gene is expressed in *E. coli* and is able to **functionally complement** the *E. coli* DNA gyrase B subunit. Expression of PAO1 *gyrA* in *E. coli* or *P. aeruginosa* with mutationally altered *gyrA* genes caused a reversion to wild-type quinolone susceptibility, indicating that the intrinsic susceptibility of the PAO1 GyrA to quinolones is comparable to that of the *E. coli* enzyme. PCR was used to amplify 360 bp of *P. aeruginosa gyrA* encompassing the so-called quinolone resistance-determining region from ciprofloxacin-resistant clinical isolates from patients with cystic fibrosis. Mutations were found in three of nine isolates tested; these mutations caused the following alterations in the sequence of GyrA: Asp at position 87 (Asp-87) to Asn, Asp-87 to Tyr, and Thr-83 to Ile. The resistance mechanisms in the other six isolates are unknown. The results of the study suggested that mechanisms other than a mutational alteration in *gyrA* are the most common mechanism of ciprofloxacin resistance in *P. aeruginosa* from the lungs of patients with cystic fibrosis.

L26 ANSWER 13 OF 36 MEDLINE
 ACCESSION NUMBER: 95348093 MEDLINE
 DOCUMENT NUMBER: 95348093 PubMed ID: 7622480
 TITLE: OpuA, an osmotically regulated binding protein-dependent transport system for the osmoprotectant glycine betaine in *Bacillus subtilis*.
 AUTHOR: Kempf B; Bremer E
 CORPORATE SOURCE: Max-Planck-Institute for Terrestrial Microbiology, Marburg, Germany.
 SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (1995 Jul 14) 270 (28) 16701-13.
 Journal code: HIV; 2985121R. ISSN: 0021-9258.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-U17292
 ENTRY MONTH: 199508
 ENTRY DATE: Entered STN: 19950911
 Last Updated on STN: 19990129
 Entered Medline: 19950825

AB Exogenously provided glycine betaine can efficiently protect *Bacillus subtilis* from the detrimental effects of high osmolarity environments. Through **functional complementation** of an *Escherichia coli* mutant deficient in glycine betaine uptake with a gene library from *B. subtilis*, we have identified a multicomponent glycine betaine transport system, OpuA. Uptake of radiolabeled glycine betaine in *B. subtilis* was found to be osmotically stimulated and was strongly decreased in a mutant strain lacking the OpuA transport system. DNA sequence analysis revealed that the components of the OpuA system are encoded by an operon (*opuA*) comprising three structural genes: *opuAA*, *opuAB*, and *opuAC*. The products of these genes exhibit features characteristic for binding protein-dependent transport systems and in particular show homology to the glycine betaine uptake system ProU

from *E. coli*. Expression of the *opuA* operon is under osmotic control. The transcriptional initiation sites of *opuA* were mapped by high resolution primer extension analysis, and two *opuA* mRNAs were detected that differed by 38 base pairs at their 5' ends. Synthesis of the shorter transcript was strongly increased in cells grown at high osmolarity, whereas the amount of the longer transcript did not vary in response to medium osmolarity. Physical and genetic mapping experiments allowed the positioning of the *opuA* operon at 25 degrees on the genetic map of *B. subtilis*.

L26 ANSWER 12 OF 36 MEDLINE
 ACCESSION NUMBER: 95369709 MEDLINE
 DOCUMENT NUMBER: 95369709 PubMed ID: 7642114
 TITLE: Isolation of cDNAs encoding GTP cyclohydrolase II from

Arabidopsis thaliana.
 AUTHOR: Kobayashi M; Sugiyama M; Yamamoto K
 CORPORATE SOURCE: Biological Institute, Faculty of Science, Tohoku University, Sendai, Japan.
 SOURCE: GENE, (1995 Jul 28) 160 (2) 303-4.
 Journal code: FOP; 7706761. ISSN: 0378-1119.
 PUB. COUNTRY: Netherlands
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-D45165
 ENTRY MONTH: 199509
 ENTRY DATE: Entered STN: 19950930
 Last Updated on STN: 19950930
 Entered Medline: 19950921

AB A GTP cyclohydrolase II-encoding gene from *Arabidopsis thaliana* was isolated through **functional complementation** of a mutant of *Escherichia coli*, BSV18, deficient in this protein. The derived amino-acid sequence constitutes a polypeptide of 27 kDa and shows 37-58% identity with previously published sequences of *Escherichia coli*, *Bacillus subtilis*, *Photobacterium leiognathi* and *P. phosphoreum*.

L26 ANSWER 11 OF 36 MEDLINE
 ACCESSION NUMBER: 95383715 MEDLINE
 DOCUMENT NUMBER: 95383715 PubMed ID: 7655065
 TITLE: A new *Bradyrhizobium japonicum* gene required for free-living growth and bacteroid development is conserved in other bacteria and in plants.
 AUTHOR: Weidenhaupt M; Schmid-Appert M; Thony B; Hennecke H; Fischer H M
 CORPORATE SOURCE: Mikrobiologisches Institut, Eidgenossische Technische Hochschule, ETH-Zentrum, Zurich, Switzerland.
 SOURCE: MOLECULAR PLANT-MICROBE INTERACTIONS, (1995 May-Jun) 8 (3) 454-64.
 Journal code: A9P; 9107902. ISSN: 0894-0282.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-L34743; GENBANK-X54385; GENBANK-Z17610
 ENTRY MONTH: 199510
 ENTRY DATE: Entered STN: 19951013
 Last Updated on STN: 19990129
 Entered Medline: 19951004

AB In the nitrogen-fixing soybean symbiont *Bradyrhizobium japonicum*, a new

DNA region, *orf74*, was discovered which is required for optimal free-living growth and, by consequence, also necessary for the formation of an effective symbiosis. A Tn5-233 insertion of *orf14* resulted in a mutant, strain 74, that has a reduced growth rate in free-living cultures under all conditions tested and less than 1% residual symbiotic nitrogen fixation activity as compared with the wild type. Nodule distribution and nodule morphology are severely affected similarly as in a previously characterized *B. japonicum* *nifA* mutant. Protein databank searches revealed

that the 142-amino-acid protein encoded by *orf74* is homologous to a 161-amino-acid protein encoded by *orf17* of *Bacillus subtilis* (approximately 46% identity; J. C. R. Struck, R. Kretschmer-Kazemi Far, W.

Schroder, F. Hucho, H. Y. Toschka, and V. A. Erdmann, *Biochim. Biophys.*

Acta, 1050:80-83, 1990) as well as to a 178-amino-acid protein encoded by

orf178 of *Escherichia coli* (approximately 45% identity; K. L. Poulsen, N.

W. Larsen, S. Molin, and P. Andersson, *Mol. Microbiol.*, 6:895-905, 1992).

Significant similarity was also found with unknown ORFs of two plant species. When expressed from a strong constitutive promoter, *orf17* of *B.*

subtilis could partially complement *B. japonicum* mutant 74. By contrast, *orf74* of *B. japonicum* was unable to functionally complement an *E. coli* *orf178* mutant. The conservation of this DNA region in gram-negative and gram-positive bacteria suggests that the gene

is essential for a fundamental cellular process which is required in *B. japonicum* for both free-living and symbiotic growth.

L26 ANSWER 9 OF 36 MEDLINE

ACCESSION NUMBER: 96013068 MEDLINE

DOCUMENT NUMBER: 96013068 PubMed ID: 7557338

TITLE: Functional characterization of the *Staphylococcus carnosus*

SecA protein in *Escherichia coli* and *Bacillus subtilis* *secA* mutant strains.

AUTHOR: Klein M; Meens J; Freudl R

CORPORATE SOURCE: Institut für Biotechnologie 1, Forschungszentrum Jülich GmbH, Germany.

SOURCE: FEMS MICROBIOLOGY LETTERS, (1995 Sep 15) 131 (3) 271-7.

Journal code: FML; 7705721. ISSN: 0378-1097.

PUB. COUNTRY: Netherlands

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

OTHER SOURCE: GENBANK-D10279; GENBANK-D90218; GENBANK-L32090;

GENBANK-M20791; GENBANK-U06928; GENBANK-X64705;

GENBANK-X65961; GENBANK-X74592; GENBANK-X79725;

GENBANK-Z35718

ENTRY-MONTH: 199510

ENTRY DATE: Entered STN: 19951227

Last Updated on STN: 19951227

Entered Medline: 19951026

AB The *Staphylococcus carnosus* *secA* gene was cloned using the *Bacillus*

subtilis *secA* gene as a probe. The *S. carnosus* *secA* encodes a polypeptide of 844 amino acid residues which is homologous to other known

SecA proteins. The *S. carnosus* *SecA* functionally

complemented the growth and secretion defects of a temperature-sensitive *B. subtilis* *secA* mutant at the non-permissive temperature. In contrast, the growth defect of an *Escherichia coli* *secA* mutant could not be complemented by the *S. carnosus*

SecA protein. Our results suggest that the interactions of *SecA* with precursor proteins and/or other components of bacterial preprotein translocase are optimized within each organism.

L26 ANSWER 6 OF 36 MEDLINE

ACCESSION NUMBER: 96224138 MEDLINE

DOCUMENT NUMBER: 96224138 PubMed ID: 8621563

TITLE: Cloning and characterization of the yeast HEM14 gene coding

for protoporphyrinogen oxidase, the molecular target of diphenyl ether-type herbicides.

AUTHOR: Camadro J M; Labbe P

CORPORATE SOURCE: Laboratoire de Biochimie des Porphyrines, Departement de

Microbiologie, Institut Jacques Monod, 2 Place Jussieu, F-75251 Paris Cedex 05, France.

SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (1996 Apr 12) 271 (15) 9120-8.

Journal code: HIV; 2985121R. ISSN: 0021-9258.

PUB. COUNTRY: United States

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

OTHER SOURCE: GENBANK-Z71381

ENTRY MONTH: 199606

ENTRY DATE: Entered STN: 19960627

Last Updated on STN: 19980206

Entered Medline: 19960620

AB Protoporphyrinogen oxidase, which catalyzes the oxygen-dependent

aromatization of protoporphyrinogen IX to protoporphyrin IX, is the molecular target of diphenyl ether type herbicides. The structural gene

for the yeast protoporphyrinogen oxidase, HEM14, was isolated by functional complementation of a *hem14-1* protoporphyrinogen oxidase-deficient yeast mutant, using a novel one-step

colored screening procedure to identify heme-synthesizing cells. The *hem14-1* mutation was genetically linked to *URA3*, a marker on chromosome V,

and HEM14 was physically mapped on the right arm of this chromosome,

between *PRP22* and *FAA2*. Disruption of the HEM14 gene leads to protoporphyrinogen oxidase deficiency in vivo (heme deficiency and accumulation of heme precursors), and in vitro (lack of immunodetectable

protein or enzyme activity). The HEM14 gene encodes a 539-amino acid

protein (59,665 Da; pI 9.3) containing an ADP- beta alpha beta-binding

fold similar to those of several other flavoproteins. Yeast protoporphyrinogen oxidase was somewhat similar to the HemY gene product

of *Bacillus subtilis* and to the human and mouse protoporphyrinogen oxidases. Studies on protoporphyrinogen oxidase overexpressed in yeast and purified as wild-type enzyme showed that

(i) the NH2-terminal mitochondrial targeting sequence of protoporphyrinogen

oxidase is not cleaved during importation; (ii) the enzyme, as purified,

had a typical flavin semiquinone absorption spectrum; and (iii) the enzyme

was strongly inhibited by diphenyl ether-type herbicides and readily photolabeled by a diazoketone derivative of tritiated acifluorfen. The mutant allele *hem14-1* contains two mutations, L422P and K424E, responsible

for the inactive enzyme. Both mutations introduced independently in

the wild-type HEM14 gene completely inactivated the protein when analyzed in an *Escherichia coli* expression system.

L26 ANSWER 5 OF 36 MEDLINE
ACCESSION NUMBER: 96359357 MEDLINE
DOCUMENT NUMBER: 96359357 PubMed ID: 8752321
TITLE: Three transport systems for the osmoprotectant glycine betaine operate in *Bacillus subtilis*: characterization of OpuD.
AUTHOR: Kappes R M; Kempf B; Bremer E
CORPORATE SOURCE: Max Planck Institute for Terrestrial Microbiology, Marburg, Germany.
SOURCE: JOURNAL OF BACTERIOLOGY, (1996 Sep) 178 (17) 5071-9.
Journal code: HH3; 2985120R. ISSN: 0021-9193.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF008220; GENBANK-U50082
ENTRY MONTH: 199611
ENTRY DATE: Entered STN: 19961219
Last Updated on STN: 2000303
Entered Medline: 19961107

AB The accumulation of the osmoprotectant glycine betaine from exogenous sources provides a high degree of osmotic tolerance to *Bacillus subtilis*. We have identified, through functional complementation of an *Escherichia coli* mutant defective in glycine betaine uptake, a new glycine betaine transport system from *B. subtilis*. The DNA sequence of a 2,310-bp segment of the cloned region revealed a single gene (*opuD*) whose product (*OpuD*) was essential for glycine betaine uptake and osmoprotection in *E. coli*. The *opuD* gene encodes a hydrophobic 56.13-kDa protein (512 amino acid residues). *OpuD* shows a significant degree of sequence identity to the choline transporter BetT and the carnitine transporter CaiT from *E. coli* and a BetT-like protein from *Haemophilus influenzae*. These membrane proteins form a family of transporters involved in the uptake of trimethylammonium compounds. The *OpuD*-mediated glycine betaine transport activity in *B. subtilis* is controlled by the environmental osmolarity. High osmolarity stimulates de novo synthesis of *OpuD* and activates preexisting *OpuD* proteins to achieve maximal glycine betaine uptake activity. An *opuD* mutant was constructed by marker replacement, and the *OpuD*-mediated glycine betaine uptake activity was compared with that of the previously identified multicomponent *OpuA* and *OpuC* (ProU) glycine betaine uptake systems. In addition, a set of mutants was constructed, each of which synthesized only one of the three glycine betaine uptake systems. These mutants were used to determine the kinetic parameters for glycine betaine transport through *OpuA*, *OpuC*, and *OpuD*. Each of these uptake systems shows high substrate affinity, with *K_m* values in the low micromolar range, which should allow *B. subtilis* to efficiently acquire the osmoprotectant from the environment. The systems differed in their contribution to the overall glycine betaine accumulation and osmoprotection. A triple *opuA*, *opuC*, and *opuD* mutant strain was isolated, and it showed no glycine betaine

uptake activity, demonstrating that three transport systems for this osmoprotectant operate in *B. subtilis*.

L26 ANSWER 3 OF 36 MEDLINE
ACCESSION NUMBER: 1998037520 MEDLINE
DOCUMENT NUMBER: 98037520 PubMed ID: 9371469
TITLE: Characterization of *Bacillus subtilis* hemN.
AUTHOR: Hippler B; Homuth G; Hoffmann T; Hungerer C; Schumann W; Jahn D
CORPORATE SOURCE: Abteilung Biochemie, Max-Planck-Institut für Terrestrische Mikrobiologie, Marburg, Germany.
SOURCE: JOURNAL OF BACTERIOLOGY, (1997 Nov) 179 (22) 7181-5.
Journal code: HH3; 2985120R. ISSN: 0021-9193.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199712
ENTRY DATE: Entered STN: 19980109
Last Updated on STN: 19980109
Entered Medline: 19971212

AB A recently cloned *Bacillus subtilis* open reading frame (*hemN*) upstream of the *dnaK* operon was identified as encoding a protein involved in oxygen-independent coproporphyrinogen III decarboxylation. *B. subtilis* hemN functionally complemented two *Salmonella typhimurium* hemF hemN double mutants under aerobic and anaerobic conditions. A *B. subtilis* hemN mutant accumulated coproporphyrinogen III only under anaerobic conditions. Interestingly, growth experiments using the *B. subtilis* hemN mutant revealed normal aerobic and anaerobic growth, indicating the presence of an alternative oxygen-independent enzymatic system. Northern blot experiments identified hemN mRNA as part of an approximately 7-kb pentacistronic transcript consisting of *lepA*, *hemN*, *hrcA*, *grpE*, and *dnaK*. One potential start site for aerobic and anaerobic transcription was located 37 bp upstream of the translational start codon of *lepA*. Comparable amounts of hemN transcript were observed under aerobic and anaerobic growth conditions. No experimental evidence for the presence of hemF in *B. subtilis* was obtained. Moreover, *B. subtilis* hemY did not substitute for hemF hemN deficiency in *S. typhimurium*. These results indicate the absence of hemF and suggest the presence of a second hemN-like gene in *B. subtilis*.

=> D HIS

(FILE 'HOME' ENTERED AT 12:48:41 ON 24 MAY 2002)

FILE 'REGISTRY' ENTERED AT 12:49:49 ON 24 MAY 2002
E "SPOIII"/CN 25

L1 1 S E4
E "SPOOJ"/CN 25
L2 1 S E4

INDEX 'ADISALERTS, ADISINSIGHT', ADISNEWS, AGRICOLA, ANABSTR, AQUASCI, BIOBUSINESS, BIOCOMMERCE, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CANCERLIT, CAPLUS, CEABA-VTB, CEN, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DRUGB, DRUGLAUNCH, DRUGMONOG2, ...'
ENTERED AT 12:53:52 ON
24 MAY 2002

E "PROKARYOTE"/CN 25
E "BACTERIUM"/CN 25

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FILE 'MEDLINE, BIOSIS, CAPLUS' ENTERED AT 13:33:15 ON
24 MAY 2002
L17      400 S L16
L18      70987 S SUBTILIS
L19      4 S L17 AND L18
L20      556256 S COMPLEMENT?
L21      3739694 S FUNCTION?
L22      0 S L20(W)L21
L23      4121 S L20(A)L21
L24      106 S L18 AND L23
L25      46 DUP REM L24 (60 DUPLICATES REMOVED)
L26      36 S L25 NOT PY>1998
L27      38 S L9 AND L23
L28      17 DUP REM L27 (21 DUPLICATES REMOVED)

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=> LOG HOLD			
COST IN U.S. DOLLARS		SINCE FILE	TOTAL
	ENTRY	SESSION	
FULL ESTIMATED COST		80.73	136.27
DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)			
SINCE FILE	TOTAL		
	ENTRY	SESSION	
CA SUBSCRIBER PRICE		-2.48	-3.10

SESSION WILL BE HELD FOR 60 MINUTES
STN INTERNATIONAL SESSION SUSPENDED AT 14:23:06 ON 24
MAY 2002

Connecting via Winsock to STN

Welcome to STN International! Enter x:x

LOGNID:SSSPTA1636DXS

PASSWORD:
***** RECONNECTED TO STN INTERNATIONAL. *****
SESSION RESUMED IN FILE 'MEDLINE, BIOSIS, CAPLUS' AT
14:59:05 ON 24 MAY 2002
FILE 'MEDLINE' ENTERED AT 14:59:05 ON 24 MAY 2002
FILE 'BIOSIS' ENTERED AT 14:59:05 ON 24 MAY 2002
COPYRIGHT (C) 2002 BIOLOGICAL ABSTRACTS INC.(R)
FILE 'CAPLUS' ENTERED AT 14:59:05 ON 24 MAY 2002
COPYRIGHT (C) 2002 AMERICAN CHEMICAL SOCIETY (ACS)

COST IN U.S. DOLLARS	ENTRY	SINCE FILE SESSION	TOTAL
FULL ESTIMATED COST		80.73	136.27
DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)			
SINCE FILE	TOTAL	ENTRY	SESSION
CA SUBSCRIBER PRICE		-2.48	-3.10

\Rightarrow d his

(FILE 'HOME' ENTERED AT 12:48:41 ON 24 MAY 2002)

FILE 'REGISTRY' ENTERED AT 12:49:49 ON 24 MAY 2002
 E "SPOIIIH"/CN 25
 L1 1 S E4
 E "SPOOJ"/CN 25
 L2 1 S E4

INDEX 'ADISALERTS, ADISINSIGHT, ADISNEWS,
AGRICOLA, ANABSTR, AQUASCI,
BIOBUSINESS, BIOCOMMERCE, BIOSIS, BIOTECHABS,
BIOTECHDS, BIOTECHNO, CABA,
CANCERLIT, CAPLUS, CEABA-VTB, CEN, CIN, CONFSCI,

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SEA SPOOJ
-----
27 FILE BIOSIS
 4 FILE BIOTECHABS
 4 FILE BIOTECHDS
16 FILE BIOTECHNO
 1 FILE CABA
19 FILE CAPLUS
15 FILE EMBASE
10 FILE ESBIODBASE
 1 FILE FEDRIP
 1 FILE FSTA
11 FILE GENBANK
 2 FILE IFIPAT
 1 FILE JICST-EPLUS
13 FILE LIFESCI
10 FILE MEDLINE
 2 FILE PASCAL
13 FILE SCISEARCH
 8 FILE TOXCENTER
 9 FILE USPATFULL
 2 FILE WPIDS
 2 FILE WPINDEX
L4   QUE SPOOJ

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FILE 'BIOSIS, CAPLUS' ENTERED AT 12:55:42 ON 24 MAY
2002
L5      97 S SPOIIIIE
L6      46 S SPOOJ
L7      3 S L5 AND L6
L8      3 DUP REM L7 (0 DUPLICATES REMOVED)
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FILE 'MEDLINE, CAPLUS, BIOSIS' ENTERED AT 13:26:26 ON
24 MAY 2002
L9   45878 S REPORTER GENE
L10  317475 S COMPLEMENTA?
L11  2166 S L9 AND L10
L12  822 S L9(P)L10
L13  6401 S SIGMA FACTOR
L14  2900 S SIGMA F
L15  0 S L12 AND L14
L16  400 DUP REM L12 (422 DUPLICATES REMOVED)

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FILE 'REGISTRY' ENTERED AT 13:31:57 ON 24 MAY 2002

CROPB, CROPU, DDFB,
DDFU, DGENE, DRUGB, DRUGLAUNCH, DRUGMONOG2, ...'
ENTERED AT 12:53:52 ON

24 MAY 2002

SEA SPOIIE

1 FILE AQUASCI
47 FILE BIOSIS
6 FILE BIOTECHABS
6 FILE BIOTECHDS
28 FILE BIOTECHNO
1 FILE CABA
50 FILE CAPLUS
1 FILE CEABA-VTB
1 FILE CONFSCI
6 FILE DGENE
30 FILE EMBASE
23 FILE ESBIODASE
3 FILE FSTA
54 FILE GENBANK
8 FILE IFIPAT
5 FILE JICST-EPLUS
34 FILE LIFESCI
37 FILE MEDLINE
9 FILE PASCAL
2 FILE PROMT
34 FILE SCISEARCH
8 FILE TOXCENTER
17 FILE USPATFULL
5 FILE WPIDS
5 FILE WPINDEX
L3 QUE SPOIIE

SEA SPOOJ

27 FILE BIOSIS
4 FILE BIOTECHABS
4 FILE BIOTECHDS
16 FILE BIOTECHNO
1 FILE CABA
19 FILE CAPLUS
15 FILE EMBASE
10 FILE ESBIODASE
1 FILE FEDRIP
1 FILE FSTA
11 FILE GENBANK
2 FILE IFIPAT
1 FILE JICST-EPLUS
13 FILE LIFESCI
10 FILE MEDLINE
2 FILE PASCAL
13 FILE SCISEARCH
8 FILE TOXCENTER
9 FILE USPATFULL
2 FILE WPIDS
2 FILE WPINDEX
L4 QUE SPOOJ

L4

FILE 'BIOSIS, CAPLUS' ENTERED AT 12:55:42 ON 24 MAY
2002

L5 97 S SPOIIE
L6 46 S SPOOJ
L7 3 S L5 AND L6
L8 3 DUP REM L7 (0 DUPLICATES REMOVED)

FILE 'MEDLINE, CAPLUS, BIOSIS' ENTERED AT 13:26:26 ON
24 MAY 2002

L9 45878 S REPORTER GENE
L10 317475 S COMPLEMENTA?
L11 2166 S L9 AND L10
L12 822 S L9(P)L10
L13 6401 S SIGMA FACTOR
L14 2900 S SIGMA F

L15 0 S L12 AND L14
L16 400 DUP REM L12 (422 DUPLICATES REMOVED)

FILE 'REGISTRY' ENTERED AT 13:31:57 ON 24 MAY 2002
E "PROKARYOTE"/CN 25
E "BACTERIUM"/CN 25

FILE 'MEDLINE, BIOSIS, CAPLUS' ENTERED AT 13:33:15 ON
24 MAY 2002

L17 400 S L16
L18 70987 S SUBTILIS
L19 4 S L17 AND L18
L20 556256 S COMPLEMENT?
L21 3739694 S FUNCTION?
L22 0 S L20(W)L21
L23 4121 S L20(A)L21
L24 106 S L18 AND L23
L25 46 DUP REM L24 (60 DUPLICATES REMOVED)
L26 36 S L25 NOT PY>1998
L27 38 S L9 AND L23
L28 17 DUP REM L27 (21 DUPLICATES REMOVED)

=> l20(3a)l21
L20(3A)L21 IS NOT A RECOGNIZED COMMAND
The previous command name entered was not recognized by the system.
For a list of commands available to you in the current file, enter
"HELP COMMANDS" at an arrow prompt (=>).

=> s l20(3a)l21
L29 9901 L20(3A) L21

=> s spoiie?
L30 137 SPOIIE?

=> s l29 and l30
L31 0 L29 AND L30

=> s spooj
L32 56 SPOOJ

=> s l29 and l32
L33 0 L29 AND L32

=> s spoiii
L34 20 SPOIII

=> s antibiotic?
L35 458251 ANTIBIOTIC?

=> s l32 and l35
L36 2 L32 AND L35

=> d ti 1-2

L36 ANSWER 1 OF 2 BIOSIS COPYRIGHT 2002 BIOLOGICAL
ABSTRACTS INC.
TI Bacillus strain and **antibiotic** screening method.

L36 ANSWER 2 OF 2 CAPLUS COPYRIGHT 2002 ACS
TI Mutant Bacillus strain and **antibiotic** screening method

=> d ibib ab 1-2

L36 ANSWER 1 OF 2 BIOSIS COPYRIGHT 2002 BIOLOGICAL
ABSTRACTS INC.

ACCESSION NUMBER: 2002:278073 BIOSIS
DOCUMENT NUMBER: PREV200200278073

TITLE: Bacillus strain and **antibiotic** screening method.

AUTHOR(S): Errington, Jeffery (1); Wu, Ling Juan

CORPORATE SOURCE: (1) Oxford UK

ASSIGNEE: ISIS Innovation Limited, Oxford, UK

PATENT INFORMATION: US 6350587 February 26, 2002

SOURCE: Official Gazette of the United States Patent and

Trademark

Office Patents, (Feb. 26, 2002) Vol. 1255, No. 4, pp. No
Pagination. <http://www.uspto.gov/web/menu/patdata.html>.
e-file.

ISSN: 0098-1133.

DOCUMENT TYPE: Patent

LANGUAGE: English

AB A Bacillus strain has a chromosome with the following
modifications: a

mutation of a spoIIIE gene which blocks transfer of the prespore
chromosome; a mutation which prevents loss of SpoOJ function
from blocking sporulation; a first reporter gene dependent on sigmaF
factor and placed at a location where impaired SpoOJ function
leads to increased trapping in the prespore; and a second reporter
gene

having a promoter which is dependent on sigmaF factor and where
impaired

SpoOJ function leads to reduced trapping in the prespore. The
strain is useful in a method of screening for putative antibiotics

L36 ANSWER 2 OF 2 CAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 1998:406093 CAPLUS

DOCUMENT NUMBER: 129:64024

TITLE: Mutant Bacillus strain and antibiotic
screening method

INVENTOR(S): Errington, Jeffery; Wu, Ling Juan

PATENT ASSIGNEE(S): Isis Innovation Ltd., UK; Errington,
Jeffery, Wu, Ling
Juan

SOURCE: PCT Int. Appl., 16 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9826087	A1	19980618	WO 1997-GB3401	19971210
W: JP, US				
RW: AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
EP 944734	A1	19990929	EP 1997-947811	19971210
R: BE, DE, ES, FR, GB, IT, NL				
JP 2001505776	T2	20010508	JP 1998-526366	19971210
US 6350587	B1	20020226	US 1999-319777	19990611
US 2002058297	A1	20020516	US 2001-26828	20011227
PRIORITY APPLN. INFO.: GB 1996-25825 A 19961212				
WO 1997-GB3401 W 19971210				
US 1999-319777 A3 19990611				

AB A Bacillus strain has a chromosome with the following
modifications: a

mutation of a spoIIIE gene which blocks transfer of the prespore
chromosome; a mutation which prevents loss of SpoOJ function
from blocking sporulation; a first reporter gene dependent on
.sigma.F

factor and placed at a location where impaired SpoOJ function
leads to increased trapping in the prespore; and a second reporter
gene

having a promoter which is dependent on .sigma.F factor and where
impaired

SpoOJ function leads to reduced trapping in the prespore. The
strain is useful in a method of screening for putative antibiotics
. The reporter genes lacZ and gus encode different detectable

enzymes,

.beta.-galactosidase and .beta.-glucuronidase, resp. The Bacillus
bacteria is killed by contact with a substance which inhibits SpoJ
function.

=> d ti l32 1-10

L32 ANSWER 1 OF 56 MEDLINE

TI Analyzing DNA strand compositional asymmetry to identify
candidate

replication origins of Borrelia burgdorferi linear and circular
plasmids.

L32 ANSWER 2 OF 56 MEDLINE

TI Penicillin-binding protein-related factor A is required for proper
chromosome segregation in Bacillus subtilis.

L32 ANSWER 3 OF 56 MEDLINE

TI Gene organization in the trxA/B-oriC region of the Streptomyces
coelicolor
chromosome and comparison with other eubacteria.

L32 ANSWER 4 OF 56 MEDLINE

TI DNA polymerase template switching at specific sites on the phi29
genome
causes the in vivo accumulation of subgenomic phi29 DNA
molecules.

L32 ANSWER 5 OF 56 MEDLINE

TI A Bacillus subtilis gene-encoding protein homologous to eukaryotic
SMC
motor protein is necessary for chromosome partition.

L32 ANSWER 6 OF 56 MEDLINE

TI Organization around the dna A gene of Streptococcus pneumoniae.

L32 ANSWER 7 OF 56 MEDLINE

TI Direct evidence for active segregation of oriC regions of the
Bacillus
subtilis chromosome and co-localization with the SpoOJ
partitioning protein.

L32 ANSWER 8 OF 56 MEDLINE

TI Roa307, a protein encoded on Coxiella burnetii plasmid QpH1,
shows
homology to proteins encoded in the replication origin region of
bacterial
chromosomes.

L32 ANSWER 9 OF 56 MEDLINE

TI spoOJ is required for normal chromosome segregation as well as the
initiation of sporulation in Bacillus subtilis.

L32 ANSWER 10 OF 56 MEDLINE

TI Cloning of the Bacillus subtilis recF gene.

=> d ibib ab 9

2 ANSWERS ARE AVAILABLE. SPECIFIED ANSWER
NUMBER EXCEEDS ANSWER SET SIZE

The answer numbers requested are not in the answer set.

ENTER ANSWER NUMBER OR RANGE (1):end

=> d ibib ab l32 9

L32 ANSWER 9 OF 56 MEDLINE

ACCESSION NUMBER: 94350812 MEDLINE

DOCUMENT NUMBER: 94350812 PubMed ID: 8071208

TITLE: spoOJ is required for normal chromosome segregation as
well

as the initiation of sporulation in Bacillus subtilis.

AUTHOR: Ireton K; Gunther N W 4th; Grossman A D

CORPORATE SOURCE: Department of Biology, Massachusetts
Institute of

Technology, Cambridge 02139.

CONTRACT NUMBER: GM41934 (NIGMS)

SOURCE: JOURNAL OF BACTERIOLOGY, (1994 Sep) 176
(17) 5320-9.

Journal code: HH3; 2985120R. ISSN: 0021-9193.

PUB. COUNTRY: United States

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals
ENTRY MONTH: 199409
ENTRY DATE: Entered STN: 19941006
Last Updated on STN: 19970203
Entered Medline: 19940928

AB The spo0J gene of Bacillus subtilis is required for the initiation of sporulation. We show that the sporulation defect caused by null mutations in spo0J is suppressed by a null mutation in the gene located directly upstream from spo0J, soj (suppressor of spo0J). These results indicate that Soj inhibits the initiation of sporulation and that Spo0J antagonizes that inhibition. Further genetic experiments indicated that Soj ultimately affects sporulation by inhibiting the activation (phosphorylation) of the developmental transcription factor encoded by spo0A. In addition, the temperature-sensitive sporulation phenotype caused by the ftsA279 (spoIIN279) mutation was partly suppressed by the soj null mutation, indicating that FtsA might also affect the activity of Soj. Soj and Spo0J are known to be similar in sequence to a family of proteins involved in plasmid partitioning, including ParA and ParB of prophage P1, SopA and SopB of F, and IncC and KorB of RK2, spo0J was found to be required for normal chromosome partitioning as well as for sporulation. spo0J null mutants produced a significant proportion of anucleate cells during vegetative growth. The dual functions of Spo0J could provide a mechanism for regulating the initiation of sporulation in response to activity of the chromosome partition machinery.

=> log hold

COST IN U.S. DOLLARS	SINCE FILE	TOTAL
	ENTRY	SESSION
FULL ESTIMATED COST	98.44	153.98

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)
SINCE FILE TOTAL

	ENTRY	SESSION
CA SUBSCRIBER PRICE	-3.10	-3.72

SESSION WILL BE HELD FOR 60 MINUTES
STN INTERNATIONAL SESSION SUSPENDED AT 15:05:38 ON 24 MAY 2002

Connecting via Winsock to STN

Welcome to STN International! Enter x:x

LOGINID:SSSPTA1636DXS

PASSWORD:

***** RECONNECTED TO STN INTERNATIONAL *****

SESSION RESUMED IN FILE 'MEDLINE, BIOSIS, CAPLUS' AT 15:33:25 ON 24 MAY 2002

FILE 'MEDLINE' ENTERED AT 15:33:25 ON 24 MAY 2002

FILE 'BIOSIS' ENTERED AT 15:33:25 ON 24 MAY 2002

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FILE 'CAPLUS' ENTERED AT 15:33:25 ON 24 MAY 2002

COPYRIGHT (C) 2002 AMERICAN CHEMICAL SOCIETY (ACS)

COST IN U.S. DOLLARS	SINCE FILE	TOTAL
	ENTRY	SESSION
FULL ESTIMATED COST	98.44	153.98

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)
SINCE FILE TOTAL

	ENTRY	SESSION
CA SUBSCRIBER PRICE	-3.10	-3.72

=> d his

(FILE 'HOME' ENTERED AT 12:48:41 ON 24 MAY 2002)

FILE 'REGISTRY' ENTERED AT 12:49:49 ON 24 MAY 2002

	E "SPOIIE"/CN 25
L1	1 S E4
	E "SPOOJ"/CN 25
L2	1 S E4

INDEX 'ADISALERTS, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, AQUASCI, BIOBUSINESS, BIOCOMMERCE, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CANCERLIT, CAPLUS, CEABA-VTB, CEN, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DRUGB, DRUGLAUNCH, DRUGMONOG2, ...' ENTERED AT 12:53:52 ON 24 MAY 2002

SEA SPOIIE

1 FILE AQUASCI
47 FILE BIOSIS
6 FILE BIOTECHABS
6 FILE BIOTECHDS
28 FILE BIOTECHNO
1 FILE CABA
50 FILE CAPLUS
1 FILE CEABA-VTB
1 FILE CONFSCI
6 FILE DGENE
30 FILE EMBASE
23 FILE ESBIODASE
3 FILE FSTA
54 FILE GENBANK
8 FILE IFIPAT
5 FILE JICST-EPLUS
34 FILE LIFESCI
37 FILE MEDLINE
9 FILE PASCAL
2 FILE PROMT
34 FILE SCISEARCH
8 FILE TOXCENTER
17 FILE USPATFULL
5 FILE WPIDS
5 FILE WPINDEX
L3 QUE SPOIIE

SEA SPOOJ

27 FILE BIOSIS
4 FILE BIOTECHABS
4 FILE BIOTECHDS
16 FILE BIOTECHNO
1 FILE CABA
19 FILE CAPLUS
15 FILE EMBASE
10 FILE ESBIODASE
1 FILE FEDRI
1 FILE FSTA
11 FILE GENBANK
2 FILE IFIPAT
1 FILE JICST-EPLUS
13 FILE LIFESCI
10 FILE MEDLINE
2 FILE PASCAL
13 FILE SCISEARCH
8 FILE TOXCENTER
9 FILE USPATFULL

L4 2 FILE WPIDS
2 FILE WPINDEX
QUE SPOOJ

FILE 'BIOSIS, CAPLUS' ENTERED AT 12:55:42 ON 24 MAY 2002

L5 97 S SPOIIE
L6 46 S SPOOJ
L7 3 S L5 AND L6
L8 3 DUP REM L7 (0 DUPLICATES REMOVED)

FILE 'MEDLINE, CAPLUS, BIOSIS' ENTERED AT 13:26:26 ON 24 MAY 2002

L9 45878 S REPORTER GENE
L10 317475 S COMPLEMENTA?
L11 2166 S L9 AND L10
L12 822 S L9(P)L10
L13 6401 S SIGMA FACTOR
L14 2900 S SIGMA F
L15 0 S L12 AND L14
L16 400 DUP REM L12 (422 DUPLICATES REMOVED)

FILE 'REGISTRY' ENTERED AT 13:31:57 ON 24 MAY 2002
E "PROKARYOTE"/CN 25
E "BACTERIUM"/CN 25

FILE 'MEDLINE, BIOSIS, CAPLUS' ENTERED AT 13:33:15 ON 24 MAY 2002

L17 400 S L16
L18 70987 S SUBTILIS
L19 4 S L17 AND L18
L20 556256 S COMPLEMENT?
L21 3739694 S FUNCTION?
L22 0 S L20(W)L21
L23 4121 S L20(A)L21
L24 106 S L18 AND L23
L25 46 DUP REM L24 (60 DUPLICATES REMOVED)
L26 36 S L25 NOT PY>1998
L27 38 S L9 AND L23
L28 17 DUP REM L27 (21 DUPLICATES REMOVED)
L29 9901 S L20(3A)L21
L30 137 S SPOIIE?
L31 0 S L29 AND L30
L32 56 S SPOOJ
L33 0 S L29 AND L32
L34 20 S SPOIII
L35 458251 S ANTIBIOTIC?
L36 2 S L32 AND L35

=> s divib or ftsq
L37 316 DIVIB OR FTSQ

=> s divic
L38 33 DIVIC

=> s diviva
L39 44 DIVIVA

=> s ftsa
L40 506 FTSA

=> s ftsl
L41 98 FTSL

=> s mrar
L42 84 MRAR

=> s ftsz
L43 1544 FTSZ

=> s pbpb
L44 284 PBPB

=> s l37 or l38 or l39 or l40 or l41 or l42 or l43 or l44
L45 2209 L37 OR L38 OR L39 OR L40 OR L41 OR L42 OR L43
OR L44

=> s l45 not l43
L46 665 L45 NOT L43

=> s l46(p)l29
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'L157(P)L89'
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'L158(P)L90'
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'L159(P)L91'
L47 0 L46(P) L29

=> s l46 and l29
L48 0 L46 AND L29

=> s l43 and l29
L49 0 L43 AND L29

=> s genetic? complementat?
L50 13781 GENETIC? COMPLEMENTAT?

=> s l46 and l50
L51 15 L46 AND L50

=> s l43 and l50
L52 24 L43 AND L50

=> s l51 or l52
L53 39 L51 OR L52

=> dup rem l53
PROCESSING COMPLETED FOR L53
L54 29 DUP REM L53 (10 DUPLICATES REMOVED)

=> d ti so 1-29

L54 ANSWER 1 OF 29 MEDLINE
TI HscA is involved in the dynamics of FtsZ-ring formation in
Escherichia coli K12.
SO GENES TO CELLS, (2001 Sep) 6 (9) 803-14.
Journal code: 9607379. ISSN: 1356-9597.

L54 ANSWER 2 OF 29 MEDLINE
TI pbpB, a gene coding for a putative penicillin-binding protein,
is required for aerobic nitrogen fixation in the cyanobacterium
Anabaena
sp. strain PCC7120.
SO JOURNAL OF BACTERIOLOGY, (2001 Jan) 183 (2) 628-36.
Journal code: HH3. ISSN: 0021-9193.

L54 ANSWER 3 OF 29 MEDLINE DUPLICATE 1
TI Two new loci affecting cell division identified as suppressors of an
ftsQ-null mutation in Streptomyces coelicolor A3(2).
SO FEMS MICROBIOLOGY LETTERS, (2001 Aug 21) 202 (2) 251-
6.
Journal code: FML; 7705721. ISSN: 0378-1097.

L54 ANSWER 4 OF 29 MEDLINE
TI Arrest of cell division and nucleoid partition by genetic alterations
in
the sliding clamp of the replicase and in DnaA.
SO Mol Genet Genomics, (2001 Oct) 266 (2) 167-79.
Journal code: 101093320. ISSN: 1617-4615.

L54 ANSWER 5 OF 29 MEDLINE
TI whmD is an essential mycobacterial gene required for proper
septation and
cell division.
SO PROCEEDINGS OF THE NATIONAL ACADEMY OF
SCIENCES OF THE UNITED STATES OF

- AMERICA, (2000 Jul 18) 97 (15) 8554-9.
Journal code: PV3; 7505876. ISSN: 0027-8424.
- L54 ANSWER 6 OF 29 MEDLINE
TI Analysis of the essential cell division gene *ftsL* of *Bacillus subtilis* by mutagenesis and heterologous complementation.
SO JOURNAL OF BACTERIOLOGY, (2000 Oct) 182 (19) 5572-9.
Journal code: HH3. ISSN: 0021-9193.
- L54 ANSWER 7 OF 29 MEDLINE
TI Cloning and characterization of *ftsZ* and *pyrF* from the archaeon *Thermoplasma acidophilum*.
SO BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (2000 Sep 7) 275 (3) 936-45.
Journal code: 9Y8; 0372516. ISSN: 0006-291X.
- L54 ANSWER 8 OF 29 MEDLINE
TI Pea chloroplast *FtsZ* can form multimers and correct the thermosensitive defect of an *Escherichia coli ftsZ* mutant.
SO MOLECULAR AND GENERAL GENETICS, (2000 Mar) 263 (2) 213-21.
Journal code: NGP; 0125036. ISSN: 0026-8925.
- L54 ANSWER 9 OF 29 MEDLINE
TI Negative regulatory role of the *Escherichia coli hfq* gene in cell division.
SO BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (1999 Dec 20) 266 (2) 579-83.
Journal code: 9Y8; 0372516. ISSN: 0006-291X.
- L54 ANSWER 10 OF 29 MEDLINE
TI Septal localization of *FtsQ*, an essential cell division protein in *Escherichia coli*.
SO JOURNAL OF BACTERIOLOGY, (1999 Jan) 181 (2) 521-30.
Journal code: HH3; 2985120R. ISSN: 0021-9193.
- L54 ANSWER 11 OF 29 MEDLINE
TI A *murC* gene from coryneform bacteria.
SO APPLIED MICROBIOLOGY AND BIOTECHNOLOGY, (1999 Feb) 51 (2) 223-8.
Journal code: AMC; 8406612. ISSN: 0175-7598.
- L54 ANSWER 12 OF 29 MEDLINE
TI *Salmonella typhimurium* encodes an *SdiA* homolog, a putative quorum sensor of the *LuxR* family, that regulates genes on the virulence plasmid.
SO JOURNAL OF BACTERIOLOGY, (1998 Mar) 180 (5) 1185-93.
Journal code: HH3; 2985120R. ISSN: 0021-9193.
- L54 ANSWER 13 OF 29 MEDLINE
TI Characterization of *ftsZ*, the cell division gene of *Buchnera aphidicola* (endosymbiont of aphids) and detection of the product.
SO CURRENT MICROBIOLOGY, (1998 Feb) 36 (2) 85-9.
Journal code: BMW; 7808448. ISSN: 0343-8651.
- L54 ANSWER 14 OF 29 MEDLINE
TI Domain-swapping analysis of *FtsI*, *FtsL*, and *FtsQ*, bitopic membrane proteins essential for cell division in *Escherichia coli*.
SO JOURNAL OF BACTERIOLOGY, (1997 Aug) 179 (16) 5094-103.
Journal code: HH3; 2985120R. ISSN: 0021-9193.
- L54 ANSWER 15 OF 29 MEDLINE DUPLICATE 2
TI Identification, characterization, and chromosomal organization of cell division cycle genes in *Caulobacter crescentus*.
SO JOURNAL OF BACTERIOLOGY, (1997 Apr) 179 (7) 2169-80.
Journal code: HH3; 2985120R. ISSN: 0021-9193.
- L54 ANSWER 16 OF 29 MEDLINE
TI *ftsW* is an essential cell-division gene in *Escherichia coli*.
- SO MOLECULAR MICROBIOLOGY, (1997 Jun) 24 (6) 1263-73.
Journal code: MOM; 8712028. ISSN: 0950-382X.
- L54 ANSWER 17 OF 29 MEDLINE
TI Requirement of topoisomerase IV *parC* and *parE* genes for cell cycle progression and developmental regulation in *Caulobacter crescentus*.
SO MOLECULAR MICROBIOLOGY, (1997 Dec) 26 (5) 897-910.
Journal code: MOM; 8712028. ISSN: 0950-382X.
- L54 ANSWER 18 OF 29 MEDLINE
TI Characterization of a five-gene cluster required for the biogenesis of type 4 fimbriae in *Pseudomonas aeruginosa*.
SO MOLECULAR MICROBIOLOGY, (1995 May) 16 (3) 497-508.
Journal code: MOM; 8712028. ISSN: 0950-382X.
- L54 ANSWER 19 OF 29 MEDLINE
TI Cloning and sequencing of the cell division gene *pbpB*, which encodes penicillin-binding protein 2B in *Bacillus subtilis*.
SO JOURNAL OF BACTERIOLOGY, (1993 Dec) 175 (23) 7604-16.
Journal code: HH3; 2985120R. ISSN: 0021-9193.
- L54 ANSWER 20 OF 29 MEDLINE
TI *Escherichia coli mraR* gene involved in cell growth and division.
SO JOURNAL OF BACTERIOLOGY, (1992 Dec) 174 (23) 7841-3.
Journal code: HH3; 2985120R. ISSN: 0021-9193.
- L54 ANSWER 21 OF 29 MEDLINE
TI The *rcsB* gene, a positive regulator of colanic acid biosynthesis in *Escherichia coli*, is also an activator of *ftsZ* expression.
SO JOURNAL OF BACTERIOLOGY, (1992 Jun) 174 (12) 3964-71.
Journal code: HH3; 2985120R. ISSN: 0021-9193.
- L54 ANSWER 22 OF 29 MEDLINE
TI An amino-proximal domain required for the localization of *FtsQ* in the cytoplasmic membrane, and for its biological function in *Escherichia coli*.
SO MOLECULAR MICROBIOLOGY, (1992 Mar) 6 (6) 715-22.
Journal code: MOM; 8712028. ISSN: 0950-382X.
- L54 ANSWER 23 OF 29 MEDLINE
TI Cloning and characterization of a *Rhizobium meliloti* homolog of the *Escherichia coli* cell division gene *ftsZ*.
SO JOURNAL OF BACTERIOLOGY, (1991 Sep) 173 (18) 5822-30.
Journal code: HH3; 2985120R. ISSN: 0021-9193.
- L54 ANSWER 24 OF 29 MEDLINE
TI New mutations *fts-36*, *fts-33*, and *ftsW* clustered in the *mra* region of the *Escherichia coli* chromosome induce thermosensitive cell growth and division.
SO JOURNAL OF BACTERIOLOGY, (1989 Oct) 171 (10) 5523-30.
Journal code: HH3; 2985120R. ISSN: 0021-9193.
- L54 ANSWER 25 OF 29 MEDLINE
TI Cell division control in *Escherichia coli* K-12: some properties of the *ftsZ84* mutation and suppression of this mutation by the product of a newly identified gene.
SO JOURNAL OF BACTERIOLOGY, (1988 Sep) 170 (9) 4338-42.
Journal code: HH3; 2985120R. ISSN: 0021-9193.
- L54 ANSWER 26 OF 29 MEDLINE DUPLICATE 3
TI Further evidence for overlapping transcriptional units in an *Escherichia coli* cell envelope-cell division gene cluster: DNA sequence and transcriptional organization of the *ddl ftsQ* region.
SO JOURNAL OF BACTERIOLOGY, (1986 Sep) 167 (3) 809-17.
Journal code: HH3; 2985120R. ISSN: 0021-9193.
- L54 ANSWER 27 OF 29 MEDLINE DUPLICATE 4
TI DNA sequence and transcriptional organization of essential cell

division

genes *ftsQ* and *ftsA* of *Escherichia coli*: evidence for overlapping transcriptional units.

SO JOURNAL OF BACTERIOLOGY, (1984 Nov) 160 (2) 546-55.

Journal code: HH3; 2985120R. ISSN: 0021-9193.

L54 ANSWER 28 OF 29 MEDLINE

TI Coupling of DNA replication and cell division: *suIB* is an allele of *ftsZ*.

SO JOURNAL OF BACTERIOLOGY, (1983 Jun) 154 (3) 1339-46.

Journal code: HH3; 2985120R. ISSN: 0021-9193.

L54 ANSWER 29 OF 29 MEDLINE

DUPLICATE 5

TI Involvement of the *ftsA* gene product in late stages of the *Escherichia coli* cell cycle.

SO JOURNAL OF BACTERIOLOGY, (1980 Feb) 141 (2) 806-13.

Journal code: HH3; 2985120R. ISSN: 0021-9193.

=> d his

(FILE 'HOME' ENTERED AT 12:48:41 ON 24 MAY 2002)

FILE 'REGISTRY' ENTERED AT 12:49:49 ON 24 MAY 2002

E "SPOIII"/CN 25

L1 1 S E4

E "SPOOJ"/CN 25

L2 1 S E4

INDEX 'ADISALERTS, ADISINSIGHT, ADISNEWS,
AGRICOLA, ANABSTR, AQUASCI,
BIOBUSINESS, BIOCOMMERCE, BIOSIS, BIOTECHABS,
BIOTECHDS, BIOTECHNO, CABA,
CANCERLIT, CAPLUS, CEABA-VTB, CEN, CIN, CONFSCI,
CROPB, CROPU, DDFB,
DDFU, DGENE, DRUGB, DRUGLAUNCH, DRUGMONOG2, ...'
ENTERED AT 12:53:52 ON
24 MAY 2002

SEA SPOIII

1 FILE AQUASCI

47 FILE BIOSIS

6 FILE BIOTECHABS

6 FILE BIOTECHDS

28 FILE BIOTECHNO

1 FILE CABA

50 FILE CAPLUS

1 FILE CEABA-VTB

1 FILE CONFSCI

6 FILE DGENE

30 FILE EMBASE

23 FILE ESBIODASE

3 FILE FSTA

54 FILE GENBANK

8 FILE IFIPAT

5 FILE JICST-EPLUS

34 FILE LIFESCI

37 FILE MEDLINE

9 FILE PASCAL

2 FILE PROMT

34 FILE SCISEARCH

8 FILE TOXCENTER

17 FILE USPATFULL

5 FILE WPIDS

5 FILE WPINDEX

L3 QUE SPOIII

SEA SPOOJ

27 FILE BIOSIS

4 FILE BIOTECHABS

4 FILE BIOTECHDS

16 FILE BIOTECHNO

1 FILE CABA

19 FILE CAPLUS

15 FILE EMBASE

10 FILE ESBIODASE

1 FILE FEDRIP

1 FILE FSTA

11 FILE GENBANK

2 FILE IFIPAT

1 FILE JICST-EPLUS

13 FILE LIFESCI

10 FILE MEDLINE

2 FILE PASCAL

13 FILE SCISEARCH

8 FILE TOXCENTER

9 FILE USPATFULL

2 FILE WPIDS

2 FILE WPINDEX

L4 QUE SPOOJ

FILE 'BIOSIS, CAPLUS' ENTERED AT 12:55:42 ON 24 MAY 2002

L5 97 S SPOIII

L6 46 S SPOOJ

L7 3 S L5 AND L6

L8 3 DUP REM L7 (0 DUPLICATES REMOVED)

FILE 'MEDLINE, CAPLUS, BIOSIS' ENTERED AT 13:26:26 ON 24 MAY 2002

L9 45878 S REPORTER GENE

L10 317475 S COMPLEMENTA?

L11 2166 S L9 AND L10

L12 822 S L9(P)L10

L13 6401 S SIGMA FACTOR

L14 2900 S SIGMA F

L15 0 S L12 AND L14

L16 400 DUP REM L12 (422 DUPLICATES REMOVED)

FILE 'REGISTRY' ENTERED AT 13:31:57 ON 24 MAY 2002

E "PROKARYOTE"/CN 25

E "BACTERIUM"/CN 25

FILE 'MEDLINE, BIOSIS, CAPLUS' ENTERED AT 13:33:15 ON 24 MAY 2002

L17 400 S L16

L18 70987 S SUBTILIS

L19 4 S L17 AND L18

L20 556256 S COMPLEMENT?

L21 3739694 S FUNCTION?

L22 0 S L20(W)L21

L23 4121 S L20(A)L21

L24 106 S L18 AND L23

L25 46 DUP REM L24 (60 DUPLICATES REMOVED)

L26 36 S L25 NOT PY>1998

L27 38 S L9 AND L23

L28 17 DUP REM L27 (21 DUPLICATES REMOVED)

L29 9901 S L20(3A)L21

L30 137 S SPOIII?

L31 0 S L29 AND L30

L32 56 S SPOOJ

L33 0 S L29 AND L32

L34 20 S SPOIII

L35 458251 S ANTIBIOTIC?

L36 2 S L32 AND L35

L37 316 S DIVIB OR FTSQ

L38 33 S DIVIC

L39 44 S DIVIVA

L40 506 S FTSA

L41 98 S FTSL

L42 84 S MRAR

L43 1544 S FTSZ

L44 284 S PBPB

L45 2209 S L37 OR L38 OR L39 OR L40 OR L41 OR L42 OR L43 OR L44

L46 665 S L45 NOT L43

L47 0 S L46(P)L29
 L48 0 S L46 AND L29
 L49 0 S L43 AND L29
 L50 13781 S GENETIC? COMPLEMENTAT?
 L51 15 S L46 AND L50
 L52 24 S L43 AND L50
 L53 39 S L51 OR L52
 L54 29 DUP REM L53 (10 DUPLICATES REMOVED)

=> s l30 or l32
 L55 190 L30 OR L32

=> s l55 and l50
 L56 7 L55 AND L50

=> dup rem l56
 PROCESSING COMPLETED FOR L56
 L57 7 DUP REM L56 (0 DUPLICATES REMOVED)

=> d ti so 1-7

L57 ANSWER 1 OF 7 MEDLINE
 TI Penicillin-binding protein-related factor A is required for proper chromosome segregation in *Bacillus subtilis*.
 SO JOURNAL OF BACTERIOLOGY, (2000 Mar) 182 (6) 1650-8.
 Journal code: HH3; 2985120R. ISSN: 0021-9193.

L57 ANSWER 2 OF 7 MEDLINE
 TI The putative DNA translocase *SpoIIIE* is required for sporulation of the symmetrically dividing coccid species *Sporosarcina ureae*.
 SO MOLECULAR MICROBIOLOGY, (2000 Feb) 35 (3) 612-22.
 Journal code: MOM; 8712028. ISSN: 0950-382X.

L57 ANSWER 3 OF 7 MEDLINE
 TI DNA polymerase template switching at specific sites on the *phi29* genome causes the in vivo accumulation of subgenomic *phi29* DNA molecules.
 SO MOLECULAR MICROBIOLOGY, (1998 Aug) 29 (3) 787-98.
 Journal code: MOM; 8712028. ISSN: 0950-382X.

L57 ANSWER 4 OF 7 MEDLINE
 TI A mutation in the *ftsK* gene of *Escherichia coli* affects cell-cell separation, stationary-phase survival, stress adaptation, and expression of the gene encoding the stress protein *UspA*.
 SO JOURNAL OF BACTERIOLOGY, (1997 Sep) 179 (18) 5878-83.
 Journal code: HH3; 2985120R. ISSN: 0021-9193.

L57 ANSWER 5 OF 7 MEDLINE
 TI A new *Escherichia coli* cell division gene, *ftsK*.
 SO JOURNAL OF BACTERIOLOGY, (1995 Nov) 177 (21) 6211-22.
 Journal code: HH3; 2985120R. ISSN: 0021-9193.

L57 ANSWER 6 OF 7 MEDLINE
 TI Cloning and dependence pattern of the sporulation operon *spoVH*.
 SO JOURNAL OF BACTERIOLOGY, (1988 Feb) 170 (2) 802-9.
 Journal code: HH3; 2985120R. ISSN: 0021-9193.

L57 ANSWER 7 OF 7 MEDLINE
 TI Cloning of the *Bacillus subtilis* *recF* gene.
 SO GENE, (1985) 38 (1-3) 139-44.
 Journal code: FOP; 7706761. ISSN: 0378-1119.

=> d ibib ab 7,6,5

L57 ANSWER 7 OF 7 MEDLINE
 ACCESSION NUMBER: 86056970 MEDLINE
 DOCUMENT NUMBER: 86056970 PubMed ID: 3934046
 TITLE: Cloning of the *Bacillus subtilis* *recF* gene.
 AUTHOR: Lampe M F; Bott K F
 CONTRACT NUMBER: GM 07092 (NIGMS)
 GM 26399 (NIGMS)

SOURCE: GENE, (1985) 38 (1-3) 139-44.
 Journal code: FOP; 7706761. ISSN: 0378-1119.
 PUB. COUNTRY: Netherlands
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 198601
 ENTRY DATE: Entered STN: 19900321
 Last Updated on STN: 20000303
 Entered Medline: 19860121

AB A cloned DNA fragment from the *ori* region of the *Bacillus subtilis* chromosome permits three separate *recF* mutants to grow in the presence of mitomycin C (MC) and survive after ultraviolet (UV) exposure. The *recF* gene has been localized to a 2.3-kb *EcoRI*-*SalI* restriction fragment on the cloned sequences. This fragment directs expression of a 34.7-kDa protein in *Escherichia coli* maxicells. Cloned DNA containing the *recF* gene does not complement or rescue *recL*, *recM* or *spoOJ* *B. subtilis* mutants. The *B. subtilis* *recF* gene also does not complement any of several of the *E. coli* recombination-deficient (*Rec-*) mutants tested.

L57 ANSWER 6 OF 7 MEDLINE
 ACCESSION NUMBER: 88115183 MEDLINE
 DOCUMENT NUMBER: 88115183 PubMed ID: 2828324
 TITLE: Cloning and dependence pattern of the sporulation operon *spoVH*.
 AUTHOR: Cutting S M; Mandelstam J
 CORPORATE SOURCE: Department of Biochemistry, University of Oxford, United Kingdom.
 SOURCE: JOURNAL OF BACTERIOLOGY, (1988 Feb) 170 (2) 802-9.
 Journal code: HH3; 2985120R. ISSN: 0021-9193.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 198803
 ENTRY DATE: Entered STN: 19900308
 Last Updated on STN: 19900308
 Entered Medline: 19880310
 AB The *spoVH* locus, involved in the sporulation of *Bacillus subtilis*, was cloned in derivatives of the temperate bacteriophage luminal diameter 105. Two recombinant phages were obtained which contained 4.2 kilobases of chromosomal DNA. Both phages only partially complemented a mutation in the *spoVH* operon, *spoVH516*. Nevertheless, analysis of the cloned locus with integrational plasmids showed that the complete operon had been cloned. A *spoVH*'-lacZ transcriptional fusion was constructed, and this indicated that the *spoVH* operon was expressed 2.25 h after the start of sporulation. The distribution of beta-galactosidase in sporulating cells containing a *spoVH*'-lacZ fusion showed that *spoVH* was expressed in the spore compartment; lac fusion experiments were also used to study *spoVH* expression in the presence of other sporulation mutations. Expression of *spoVH* was prevented by mutations in any of the stage 0 or stage II loci and also by mutations in *spoIIIA*, *spoIIIB*, and *spoIIIE*. A similar pattern of dependence was found previously for the expression of

spoVA, which is also expressed in the spore compartment.

L57 ANSWER 5 OF 7 MEDLINE

ACCESSION NUMBER: 96042098 MEDLINE

DOCUMENT NUMBER: 96042098 PubMed ID: 7592387

TITLE: A new Escherichia coli cell division gene, *ftsK*.

AUTHOR: Begg K J; Dewar S J; Donachie W D

CORPORATE SOURCE: Institute of Cell and Molecular Biology, University of

Edinburgh, Scotland.

SOURCE: JOURNAL OF BACTERIOLOGY, (1995 Nov) 177 (21) 6211-22.

Journal code: HH3; 2985120R. ISSN: 0021-9193.

PUB. COUNTRY: United States

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

OTHER SOURCE: GENBANK-Z49932

ENTRY MONTH: 199512

ENTRY DATE: Entered STN: 19960124

Last Updated on STN: 19960124

Entered Medline: 19951207

AB A mutation in a newly discovered Escherichia coli cell division gene,

ftsK, causes a temperature-sensitive late-stage block in division but does

not affect chromosome replication or segregation. This defect is specifically suppressed by deletion of *dacA*, coding for the peptidoglycan

DD-carboxypeptidase, PBP 5. *FtsK* is a large polypeptide (147 kDa) consisting of an N-terminal domain with several predicted membrane-spanning regions, a proline-glutamine-rich domain, and a C-terminal domain with a nucleotide-binding consensus sequence.

FtsK has

extensive sequence identity with a family of proteins from a wide variety

of prokaryotes and plasmids. The plasmid proteins are required for intercellular DNA transfer, and one of the bacterial proteins (the *SpoIIIE* protein of *Bacillus subtilis*) has also been implicated in intracellular chromosomal DNA transfer.

=> d ibib ab 154 28,25,23,20,16,14

L54 ANSWER 28 OF 29 MEDLINE

ACCESSION NUMBER: 83213158 MEDLINE

DOCUMENT NUMBER: 83213158 PubMed ID: 6343351

TITLE: Coupling of DNA replication and cell division: *sulB* is an

allele of *ftsZ*.

AUTHOR: Lutkenhaus J F

CONTRACT NUMBER: GM-29764 (NIGMS)

SOURCE: JOURNAL OF BACTERIOLOGY, (1983 Jun) 154 (3) 1339-46.

Journal code: HH3; 2985120R. ISSN: 0021-9193.

PUB. COUNTRY: United States

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 198307

ENTRY DATE: Entered STN: 19900319

Last Updated on STN: 19970203

Entered Medline: 19830729

AB Treatments that damage DNA in Escherichia coli result in the inhibition of

cell division. This inhibition is controlled by the *lexA-recA* regulatory

circuit and can be specifically uncoupled by the mutations *sulA* (*sfiA*) and

sulB (*sfiB*), which map at 21 and 2 min, respectively. Presently it is thought that *sulA* codes for an inducible inhibitor of cell division, the expression of which is controlled directly by the *lexA* repressor. In this

report, it is shown that *sulB* is an allele of *ftsZ*, an essential

cell division gene. A *sulB* mutation leads to an altered *ftsZ* gene product which is slightly thermosensitive and has an altered mobility

on polyacrylamide gels. It is suggested that the altered *ftsZ* gene product is resistant to the *sulA* inhibitor, thus permitting cell division after induction of the SOS response. It is also shown that an increase in the gene dosage of *ftsZ* delays the onset of filamentation after SOS induction.

L54 ANSWER 25 OF 29 MEDLINE

ACCESSION NUMBER: 88314939 MEDLINE

DOCUMENT NUMBER: 88314939 PubMed ID: 2842315

TITLE: Cell division control in Escherichia coli K-12: some properties of the *ftsZ84* mutation and suppression of this mutation by the product of a newly identified gene.

AUTHOR: Phoenix P; Drapeau G R

CORPORATE SOURCE: Department of Microbiology and Immunology, Universite de Montreal, Quebec, Canada.

SOURCE: JOURNAL OF BACTERIOLOGY, (1988 Sep) 170 (9) 4338-42.

Journal code: HH3; 2985120R. ISSN: 0021-9193.

PUB. COUNTRY: United States

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 198810

ENTRY DATE: Entered STN: 19900308

Last Updated on STN: 19900308

Entered Medline: 19881006

AB The *Fts* proteins play an important role in the control of cell division in

Escherichia coli. These proteins, which possibly form a functional complex, are encoded by genes that form an operon. In this study, we examined the properties of the temperature-sensitive mutation *ftsZ84* harbored by low- or high-copy-number plasmids. Cells of strain

AB1157,

which had the *ftsZ84* mutation, did not form colonies on salt-free L agar

at 30 degrees C. When a low-copy-number plasmid containing the *ftsZ84*

mutation was present in these mutant cells, colony formation was restored

on this medium at 30 degrees C, suggesting that *FtsZ84* is probably less

active than the wild-type protein and is therefore limiting in its capacity to trigger cell divisions. On the other hand, when the *ftsZ84* mutation was harbored by the high-copy-number plasmid pBR325, colony

formation was prevented on salt-free L agar plates whether the recipients

were *ftsZ84* mutant or parental cells, suggesting that, at high levels, *FtsZ84* acts as a division inhibitor. The fact that colony formation was

also prevented at 42 degrees C indicates that the *FtsZ84* protein is not inactivated at the nonpermissive temperature. The possibility that *FtsZ84*

is a more efficient division inhibitor than the wild-type *FtsZ* is discussed. Evidence is also presented showing that a gene adjacent to

mutT codes for a product that, under certain conditions, suppresses the

ftsZ84 mutation.

L54 ANSWER 23 OF 29 MEDLINE

ACCESSION NUMBER: 91358375 MEDLINE

DOCUMENT NUMBER: 91358375 PubMed ID: 1653222

TITLE: Cloning and characterization of a *Rhizobium meliloti* homolog of the Escherichia coli cell division gene *ftsZ*.

AUTHOR: Margolin W; Corbo J C; Long S R

CORPORATE SOURCE: Department of Biological Sciences, Stanford University,

California 94305-5020.

SOURCE: JOURNAL OF BACTERIOLOGY, (1991 Sep) 173
(18) 5822-30.

Journal code: HH3; 2985120R. ISSN: 0021-9193.

PUB. COUNTRY: United States

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

OTHER SOURCE: GENBANK-M64126; GENBANK-M64127;

GENBANK-M64128;

GENBANK-M64129; GENBANK-M94386; GENBANK-

S52988;

GENBANK-S52991; GENBANK-S53819; GENBANK-

S53821;

GENBANK-S54126

ENTRY MONTH: 199110

ENTRY DATE: Entered STN: 19911027

Last Updated on STN: 19911027

Entered Medline: 19911009

AB The *ftsZ* gene is essential for initiation of cell division in *Escherichia coli* and *Bacillus subtilis*. To begin our studies of division

arrest during differentiation of *Rhizobium meliloti* bacteroids, we isolated a *R. meliloti ftsZ* homolog, *ftsZRm*. Degenerate primers directed towards a conserved region of *ftsZ* were used to amplify a segment of *R. meliloti* DNA by polymerase chain reaction, and the product

of this reaction was then used to isolate positive clones from a bacteriophage library. The DNA sequence of an open reading frame containing the region of homology indicated that the *R. meliloti FtsZ* protein (*FtsZRm*) is 50% homologous to the known *E. coli* and *B. subtilis FtsZ* proteins, but at 590 amino acids (63 kDa), it is predicted to be nearly 50% larger. Strong expression of an approximately 70-kDa labeled protein in a coupled in vitro transcription-translation system supports this prediction. The additional

200 amino acids appear to fall in a single internal domain highly enriched

for proline and glutamine residues. When we regulated *R. meliloti ftsZ* (*ftsZRm*) expression on a high-copy-number plasmid in *E. coli* with *Plac* and *lacIq*, cells were smaller than normal in the presence of low

FtsZRm levels (with no isopropyl-beta-D-thiogalactopyranoside [IPTG]) and

filamentous when *FtsZRm* was overproduced (with IPTG). These results

suggest that low levels of *FtsZRm* stimulate *E. coli* cell division, while

high levels may be inhibitory.

L54 ANSWER 20 OF 29 MEDLINE

ACCESSION NUMBER: 93077472 MEDLINE

DOCUMENT NUMBER: 93077472 PubMed ID: 1447153

TITLE: *Escherichia coli mraR* gene involved in cell growth and division.

AUTHOR: Ueki M; Wachi M; Jung H K; Ishino F; Matsuhashi M

CORPORATE SOURCE: Institute of Applied Microbiology, University of Tokyo, Japan.

SOURCE: JOURNAL OF BACTERIOLOGY, (1992 Dec) 174
(23) 7841-3.

Journal code: HH3; 2985120R. ISSN: 0021-9193.

PUB. COUNTRY: United States

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

OTHER SOURCE: GENBANK-L01135; GENBANK-L01136;

GENBANK-L01137;

GENBANK-L01138; GENBANK-L01139; GENBANK-

L01140;

GENBANK-L01141; GENBANK-M98391; GENBANK-

S49802;

GENBANK-Z11768

ENTRY MONTH: 199212

ENTRY DATE: Entered STN: 19930129

Last Updated on STN: 19930129

Entered Medline: 19921230

AB The *mraR* gene, which has a coding frame of 363 bp and lies close to and upstream of the *ftsI* gene of *Escherichia coli*, is involved in both

cell division and cell lysis. It is thought to function in regulating the two distinct steps of the cell cycle, as two different one-base mutations

in this unique gene caused different phenotypical changes in the cell. Comparison of nucleotide sequences of the mutant type *mraR* DNAs with the wild type suggested that filamentation of the cell was caused

by

a mutation in the putative start codon, whereas lysis of the cell was caused by a mutation which led to a change of one internal glutamate residue to lysine.

L54 ANSWER 16 OF 29 MEDLINE

ACCESSION NUMBER: 97361813 MEDLINE

DOCUMENT NUMBER: 97361813 PubMed ID: 9218774

TITLE: *ftsW* is an essential cell-division gene in *Escherichia coli*.

AUTHOR: Boyle D S; Khattar M M; Addinall S G; Lutkenhaus J;

Donachie W D

CORPORATE SOURCE: Institute of Cell and Molecular Biology, University of

Edinburgh, UK.

CONTRACT NUMBER: R01GM29764 (NIGMS)

SOURCE: MOLECULAR MICROBIOLOGY, (1997 Jun) 24 (6)
1263-73.

Journal code: MOM; 8712028. ISSN: 0950-382X.

PUB. COUNTRY: ENGLAND: United Kingdom

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 199709

ENTRY DATE: Entered STN: 19971008

Last Updated on STN: 19971008

Entered Medline: 19970923

AB In the absence of exogenous promoters, plasmid-mediated complementation of

the temperature-sensitive *ftsW201* allele requires the presence of the full

coding sequence of *ftsW* plus upstream DNA encompassing the C-terminus of

mraY and the full coding sequence of *murD*. We used molecular and genetic

techniques to introduce an insertional inactivation into the chromosomal

copy of *ftsW*, in the presence of the plasmid-borne wild-type *ftsW* gene

under the control of P(BAD). In the absence of arabinose, the *ftsW*-null

strain is not viable, and a shift from arabinose- to glucose-containing liquid medium resulted in a block in division, followed by cell lysis. Immunofluorescence microscopy revealed that in *ftsW*-null

filaments, the

FtsZ ring is absent in 50-60% of filaments, whilst between one and three Z-rings per filament can be detected in the remainder of the population, with the majority of these containing only one Z-ring per filament. We also demonstrated that the expression of only *ftsWS*

(the smaller of two *ftsW* open reading frames) from P(BAD) is sufficient for

complementation of the *ftsW*-null allele. We conclude that *FtsW* is an

essential cell-division protein in *Escherichia coli*, and that it plays a role in the stabilization of the *FtsZ* ring during cell division.

L54 ANSWER 14 OF 29 MEDLINE

ACCESSION NUMBER: 97405907 MEDLINE

DOCUMENT NUMBER: 97405907 PubMed ID: 9260951

TITLE: Domain-swapping analysis of *FtsI*, *FtsL*, and

FtsQ, bitopic membrane proteins essential for cell division in *Escherichia coli*.

AUTHOR: Guzman L M; Weiss D S; Beckwith J
 CORPORATE SOURCE: Department of Microbiology and Molecular Genetics, Harvard Medical School, Boston, Massachusetts 02115, USA.
 CONTRACT NUMBER: GM38922 (NIGMS)
 SOURCE: JOURNAL OF BACTERIOLOGY, (1997 Aug) 179 (16) 5094-103.
 Journal code: HH3; 2985120R. ISSN: 0021-9193.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 199709
 ENTRY DATE: Entered STN: 19970922
 Last Updated on STN: 19980206
 Entered Medline: 19970905

AB **FtsI**, **FtsL**, and **FtsQ** are three membrane proteins required for assembly of the division septum in the bacterium *Escherichia coli*. Cells lacking any of these three proteins form long, aseptate filaments that eventually lyse. **FtsI**, **FtsL**, and **FtsQ** are not homologous but have similar overall structures: a small cytoplasmic domain, a single membrane-spanning segment (MSS), and a large periplasmic domain that probably encodes the primary functional activities of these proteins. The periplasmic domain of **FtsI** catalyzes transpeptidation and is involved in the synthesis of septal peptidoglycan. The precise functions of **FtsL** and **FtsQ** are not known. To ask whether the cytoplasmic domain and MSS of each protein serve only as a membrane anchor or have instead a more sophisticated function, we have used molecular genetic techniques to swap these domains among the three **Fts** proteins and one membrane protein not involved in cell division, MalF. In the cases of **FtsI** and **FtsL**, replacement of the cytoplasmic domain and/or MSS resulted in the loss of the ability to support cell division. For **FtsQ**, MSS swaps supported cell division but cytoplasmic domain swaps did not. We discuss several potential interpretations of these results, including that the essential domains of **FtsI**, **FtsL**, and **FtsQ** have a role in regulating the localization and/or activity of these proteins to ensure that septum formation occurs at the right place in the cell and at the right time during the division cycle.

=> d his

(FILE 'HOME' ENTERED AT 12:48:41 ON 24 MAY 2002)

FILE 'REGISTRY' ENTERED AT 12:49:49 ON 24 MAY 2002

E "SPOIIE"/CN 25

L1 1 S E4

E "SPOOJ"/CN 25

L2 1 S E4

INDEX 'ADISALERTS, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, AQUASCI, BIOBUSINESS, BIOCOMMERCE, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO; CABA, CANCERLIT, CAPLUS, CEABA-VTB, CEN, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DRUGB, DRUGLAUNCH, DRUGMONOG2, ...' ENTERED AT 12:53:52 ON 24 MAY 2002

SEA SPOIIE

 1 FILE AQUASCI
 47 FILE BIOSIS

6 FILE BIOTECHABS
 6 FILE BIOTECHDS
 28 FILE BIOTECHNO
 1 FILE CABA
 50 FILE CAPLUS
 1 FILE CEABA-VTB
 1 FILE CONFSCI
 6 FILE DGENE
 30 FILE EMBASE
 23 FILE ESBIODBASE
 3 FILE FSTA
 54 FILE GENBANK
 8 FILE IFIPAT
 5 FILE JICST-EPLUS
 34 FILE LIFESCI
 37 FILE MEDLINE
 9 FILE PASCAL
 2 FILE PROMT
 34 FILE SCISEARCH
 8 FILE TOXCENTER
 17 FILE USPATFULL
 5 FILE WPIDS
 5 FILE WPINDEX
 QUE SPOIIE

L3

 SEA SPOOJ

27 FILE BIOSIS
 4 FILE BIOTECHABS
 4 FILE BIOTECHDS
 16 FILE BIOTECHNO
 1 FILE CABA
 19 FILE CAPLUS
 15 FILE EMBASE
 10 FILE ESBIODBASE
 1 FILE FEDRIP
 1 FILE FSTA
 11 FILE GENBANK
 2 FILE IFIPAT
 1 FILE JICST-EPLUS
 13 FILE LIFESCI
 10 FILE MEDLINE
 2 FILE PASCAL
 13 FILE SCISEARCH
 8 FILE TOXCENTER
 9 FILE USPATFULL
 2 FILE WPIDS
 2 FILE WPINDEX
 QUE SPOOJ

L4

FILE 'BIOSIS, CAPLUS' ENTERED AT 12:55:42 ON 24 MAY 2002

L5 97 S SPOIIE

L6 46 S SPOOJ

L7 3 S L5 AND L6

L8 3 DUP REM L7 (0 DUPLICATES REMOVED)

FILE 'MEDLINE, CAPLUS, BIOSIS' ENTERED AT 13:26:26 ON 24 MAY 2002

L9 45878 S REPORTER GENE

L10 317475 S COMPLEMENTA?

L11 2166 S L9 AND L10

L12 822 S L9(P)L10

L13 6401 S SIGMA FACTOR

L14 2900 S SIGMA F

L15 0 S L12 AND L14

L16 400 DUP REM L12 (422 DUPLICATES REMOVED)

FILE 'REGISTRY' ENTERED AT 13:31:57 ON 24 MAY 2002

E "PROKARYOTE"/CN 25

E "BACTERIUM"/CN 25

FILE 'MEDLINE, BIOSIS, CAPLUS' ENTERED AT 13:33:15 ON

24 MAY 2002

L17 400 S L16
 L18 70987 S SUBTILIS
 L19 4 S L17 AND L18
 L20 556256 S COMPLEMENT?
 L21 3739694 S FUNCTION?
 L22 0 S L20(W)L21
 L23 4121 S L20(A)L21
 L24 106 S L18 AND L23
 L25 46 DUP REM L24 (60 DUPLICATES REMOVED)
 L26 36 S L25 NOT PY>1998
 L27 38 S L9 AND L23
 L28 17 DUP REM L27 (21 DUPLICATES REMOVED)
 L29 9901 S L20(3A)L21
 L30 137 S SPOIIIIE?
 L31 0 S L29 AND L30
 L32 56 S SPOOJ
 L33 0 S L29 AND L32
 L34 20 S SPOIII
 L35 458251 S ANTIBIOTIC?
 L36 2 S L32 AND L35
 L37 316 S DIVIB OR FTSQ
 L38 33 S DIVIC
 L39 44 S DIVIVA
 L40 506 S FTSA
 L41 98 S FTSL
 L42 84 S MKAR
 L43 1544 S FTSZ
 L44 284 S PBPB
 L45 2209 S L37 OR L38 OR L39 OR L40 OR L41 OR L42 OR L43 OR L44
 L46 665 S L45 NOT L43
 L47 0 S L46(P)L29
 L48 0 S L46 AND L29
 L49 0 S L43 AND L29
 L50 13781 S GENETIC? COMPLEMENTAT?
 L51 15 S L46 AND L50
 L52 24 S L43 AND L50
 L53 39 S L51 OR L52
 L54 29 DUP REM L53 (10 DUPLICATES REMOVED)
 L55 190 S L30 OR L32
 L56 7 S L55 AND L50
 L57 7 DUP REM L56 (0 DUPLICATES REMOVED)

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 NEWS 7 Mar 22 TOXLIT no longer available
 NEWS 8 Mar 22 TRCTHERMO no longer available
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=> file medline

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MEDLINE thesauri in the /CN, /CT, and /MN fields incorporate the MeSH 2002 vocabulary. Enter HELP THESAURUS for details.

THIS FILE CONTAINS CAS REGISTRY NUMBERS FOR EASY AND ACCURATE SUBSTANCE IDENTIFICATION.

=> d lysol
NO L# DEFINED

=> s lysol
L1 50 LYSOL

=> s l1 not py>88
12743598 PY>88
L2 0 L1 NOT PY>88

=> s l1 not py>97
12743598 PY>97
L3 0 L1 NOT PY>97

=> file caplus
COST IN U.S. DOLLARS SINCE FILE TOTAL
ENTRY SESSION
FULL ESTIMATED COST 1.14 1.35

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=> s lysol
285 LYSOL
1 LYSOLS
L4 286 LYSOL
(LYSOL OR LYSOLS)

=> s l4 not py>97
21832315 PY>97
L5 3 L4 NOT PY>97

=> d ti so 1-3

L5 ANSWER 1 OF 3 CAPLUS COPYRIGHT 2002 ACS
TI The collection and commercial preparation of Ceara rubber (Manihot glaziovii)

SO Tanganyika Territory Dept. Agr., Pamphlet, No. 33, 4 pp.

L5 ANSWER 2 OF 3 CAPLUS COPYRIGHT 2002 ACS
TI Regomyia betae Schiffn. in Tullnerfeld
SO Listy Cukrovar., 51(No. 50), Rozhledy 25

L5 ANSWER 3 OF 3 CAPLUS COPYRIGHT 2002 ACS
TI The use of aluminum in the manufacture of equipment
SO Metallborse, 17, 985-6, 1044-5, 1100-1, 1157, 1213-4, 1269, 1380-1, 1491-2, 1547-8
From: Chem. Zentr. 1927, II, 1075-6

=> s antiseptic
7007 ANTISEPTIC
41162 ANTISEPTICS
L6 46435 ANTISEPTIC
(ANTISEPTIC OR ANTISEPTICS)

=> s kill?
L7 98229 KILL?

=> s l6 and l7
L8 1054 L6 AND L7

=> s l8 not py>97
21832315 PY>97
L9 1 L8 NOT PY>97

=> s l8 not py>1997
3930480 PY>1997
L10 984 L8 NOT PY>1997

=> s l4 not py>1997
3930480 PY>1997
L11 280 L4 NOT PY>1997

=> d ti so 1-10

L11 ANSWER 1 OF 280 CAPLUS COPYRIGHT 2002 ACS
TI Lipsticks containing sucrose benzoic acid esters and cyclic silicones dispersed in amphoteric polymers
SO Jpn. Kokai Tokkyo Koho, 9 pp.
CODEN: JKXXAF

L11 ANSWER 2 OF 280 CAPLUS COPYRIGHT 2002 ACS
TI Preliminary assessment of the effect of disinfectants on skin changes in health service workers
SO Med. Pr. (1995), 46(2), 149-54
CODEN: MEPAAX; ISSN: 0465-5893

L11 ANSWER 3 OF 280 CAPLUS COPYRIGHT 2002 ACS
TI Usefulness of repellents in orchard protection against hares
SO J. Fruit Ornamental Plant Res. (1994), 2(2), 49-60
CODEN: JFOREN; ISSN: 1231-0948

L11 ANSWER 4 OF 280 CAPLUS COPYRIGHT 2002 ACS
TI Disinfectant toilet detergents
SO Faming Zhuanli Shenqing Gongkai Shuomingshu, 5 pp.
CODEN: CNXXEV

L11 ANSWER 5 OF 280 CAPLUS COPYRIGHT 2002 ACS
TI Microbial sample processing using a disinfectant for lysis
SO Can. Pat. Appl., 38 pp.
CODEN: CPXXEB

L11 ANSWER 6 OF 280 CAPLUS COPYRIGHT 2002 ACS
TI Disinfectants and lysing agents in protocol for release of intracellular components
SO Eur. Pat. Appl., 23 pp.
CODEN: EPXXDW

L11 ANSWER 7 OF 280 CAPLUS COPYRIGHT 2002 ACS
TI Chemical disinfection to interrupt transfer of rhinovirus type 14 from

environmental surfaces to hands

SO Appl. Environ. Microbiol. (1993), 59(5), 1579-85
CODEN: AEMIDF; ISSN: 0099-2240

L11 ANSWER 8 OF 280 CAPLUS COPYRIGHT 2002 ACS
TI Comparison the bactericidal and fungicidal activities of disinfectants against the pathogens isolated from poultrys

SO Zhonghua Minguo Shouyi Xuehui Zazhi (1991), 17(1), 27-35
CODEN: CKSCDN; ISSN: 0253-9179

L11 ANSWER 9 OF 280 CAPLUS COPYRIGHT 2002 ACS
TI Impact modified acrylic capstock composition for structural plastics
SO Eur. Pat. Appl., 14 pp.
CODEN: EPXXDW

L11 ANSWER 10 OF 280 CAPLUS COPYRIGHT 2002 ACS
TI Hair growth stimulant preparation containing boric acid and resorcinol
SO Fr. Demande, 6 pp.
CODEN: FRXXBL

=> d ti so 250-280

L11 ANSWER 250 OF 280 CAPLUS COPYRIGHT 2002 ACS
TI The Disinfection Value of Sprinkling with Chemicals
SO Centr. Bakt. Parasitenk, I Abt., Ref. (1913), 57, 34-5

L11 ANSWER 251 OF 280 CAPLUS COPYRIGHT 2002 ACS
TI The Disinfection Value of Sprinkling with Chemicals
SO Z. Militarärzte, Tokyo (1912), (No. 35)

L11 ANSWER 252 OF 280 CAPLUS COPYRIGHT 2002 ACS
TI Safety explosives.

L11 ANSWER 253 OF 280 CAPLUS COPYRIGHT 2002 ACS
TI The Disinfecting Action of Izal
SO Desinfektion (1913), 4, 565-77
From: Chem. Zentr., 1912, I, 1581

L11 ANSWER 254 OF 280 CAPLUS COPYRIGHT 2002 ACS
TI The Determination of the Phenol Coefficient of some Commercial Disinfectants
SO Hyg. Lab. P. H. M. H. Serv., Bull. (1912), 82, 35-74

L11 ANSWER 255 OF 280 CAPLUS COPYRIGHT 2002 ACS
TI Cauterization of the Eye with Lysol and Potassium Permanganate
SO Klin. Monatsbl. Augenheilk. (1912), 12, 758; also in Zentr. Biochem.
Biophys., 12, 697-8

L11 ANSWER 256 OF 280 CAPLUS COPYRIGHT 2002 ACS
TI In what Concentration does Alcohol Alone, or in Combination with Other Disinfectants, Kill Pus-forming Organisms?
SO Seifensieder Ztg. (1912), 39, 790

L11 ANSWER 257 OF 280 CAPLUS COPYRIGHT 2002 ACS
TI In what Concentration does Alcohol Alone, or in Combination with Other Disinfectants, Kill Pus-forming Organisms?
SO Z. Hyg. (1912), 70, 225

L11 ANSWER 258 OF 280 CAPLUS COPYRIGHT 2002 ACS
TI Mortar.

L11 ANSWER 259 OF 280 CAPLUS COPYRIGHT 2002 ACS
TI A Simple Method for Determining the Mineral Content and Hardness of Water
SO Munch. med. Wochschr. (1912), 58, 2611-3

L11 ANSWER 260 OF 280 CAPLUS COPYRIGHT 2002 ACS
TI The Antiseptic "Microsol"
SO Bull. soc. encour. ind. nat. (1911), 115, 613-27

L11 ANSWER 261 OF 280 CAPLUS COPYRIGHT 2002 ACS
TI Quantitative Determination of Phenols in the Human Organs in a Case of Lysol Poisoning
SO Schweiz Wochschr. (1911), 49, 121-2

L11 ANSWER 262 OF 280 CAPLUS COPYRIGHT 2002 ACS
TI Annual Report of the Chem. Untersuchungsamt Der Stadt Breslau, April 1, 1909 to March 31, 1910
SO Chem.-Ztg. (1911), 35, 53

L11 ANSWER 263 OF 280 CAPLUS COPYRIGHT 2002 ACS
TI Practical Helps for the Manufacture of Disinfectant Soaps
SO Seifensieder Ztg. (1911), 36, 1437-9, 1500-1, 1523-5

L11 ANSWER 264 OF 280 CAPLUS COPYRIGHT 2002 ACS
TI An Experimental Contribution on the Chemical Disinfection of Sputum Containing Tubercular Bacilli
SO Arch. Hyg. (1909), 71, 87-123

L11 ANSWER 265 OF 280 CAPLUS COPYRIGHT 2002 ACS
TI Bactericidal Action of Hydrogen Peroxide
SO Z. Hyg. (1909), 63, 319-42

L11 ANSWER 266 OF 280 CAPLUS COPYRIGHT 2002 ACS
TI Comparative Tests of the Disinfecting Action of Lysol, Liquor Cresoli Saponatus and Several Newer Disinfectants of Similar Composition
SO Disinfection (1909), 1, 267
From: Chem. Zentr., 1909, 1, 206

L11 ANSWER 267 OF 280 CAPLUS COPYRIGHT 2002 ACS
TI Two New Formaldehyde Soap Preparations
SO Disinfektion (1909), 1, 12
From: Chem. Zentr., 1908, II, 968

L11 ANSWER 268 OF 280 CAPLUS COPYRIGHT 2002 ACS
TI Diphenyloxalester, Phenol in Stable Tablet Form with Increased Disinfecting Properties
SO Hyg. Zentr. (1909), 4, 201
From: Chem. Zentr., 1908, II, 969, 1949

L11 ANSWER 269 OF 280 CAPLUS COPYRIGHT 2002 ACS
TI Lysol and Carbol Tablets and the Applicability of the Raschig Method to the Determination of m-Cresol in Cresol Tablets
SO Ber. pharm. Ges. (1909), 18, 421-30

L11 ANSWER 270 OF 280 CAPLUS COPYRIGHT 2002 ACS
TI Cresol Soap
SO Pharm.-Ztg. (1909), 53, 817, 921

L11 ANSWER 271 OF 280 CAPLUS COPYRIGHT 2002 ACS
TI The Disinfective Value of the Three Cresol Isomers in a Soap Mixture
SO Arch. Hyg. (1909), 67, 1-34

L11 ANSWER 272 OF 280 CAPLUS COPYRIGHT 2002 ACS
TI Cresol Excretion in the Dog after Lysol Administration
SO Berlin. Therap. Monatsh. (1908), 22, 366-7

L11 ANSWER 273 OF 280 CAPLUS COPYRIGHT 2002 ACS
TI On the Antiseptic Value of the New Cresol Soaps of the Ministerial Decree of Oct. 19, 1907
SO Untersuchungsamt, Stadt Berlin. Berl. klin. Wochschr. (1908), 45, 778-80

L11 ANSWER 274 OF 280 CAPLUS COPYRIGHT 2002 ACS

TI Toxicological Comparison between Chinosol, Lysol, and Cresol
SO Chem.-Ztg. (1908), 32, 23

L11 ANSWER 275 OF 280 CAPLUS COPYRIGHT 2002 ACS
TI Toxicological Comparison between Chinosol, Lysol and Cresol
SO Vierteljschr. ger. Med. [3] (1907), 34, 1-13

L11 ANSWER 276 OF 280 CAPLUS COPYRIGHT 2002 ACS
TI Experiments Concerning the Chemistry of Cresol-poisoning
SO Biochem. Z. (1908), 7, 39-44

L11 ANSWER 277 OF 280 CAPLUS COPYRIGHT 2002 ACS
TI Urine Coloration after Lysol Poisoning
SO Beitr. Chem. Physiol. (Hofmeister) (1907), 10, 251-52

L11 ANSWER 278 OF 280 CAPLUS COPYRIGHT 2002 ACS
TI Remarks and Explanations Relating to Wandel's Paper on the Pathology of Lysol and Cresol Poisoning
SO Arch. exp. Path. Pharm. (1907), 56, 416-19

L11 ANSWER 279 OF 280 CAPLUS COPYRIGHT 2002 ACS
TI Lysol and Cresol Poisoning
SO Arch. Exp. Pathol. and Pharmacol. (1907), 56, 161-86

L11 ANSWER 280 OF 280 CAPLUS COPYRIGHT 2002 ACS
TI Mouth Disinfection in the Prophylaxis and Treatment of Pneumonia
SO J. Infect. Dis. (1907), 3, 774,97

=> s lysol/ti

L12 31 LYSOL/TI

=> d ti so 1-31

L12 ANSWER 1 OF 31 CAPLUS COPYRIGHT 2002 ACS
TI Spectrophotometric estimation of cresol in cresol with soap solution I.P.
(lysol)
SO Indian J. Pharm. Sci. (1978), 40(4), 135-6
CODEN: IJSDW

L12 ANSWER 2 OF 31 CAPLUS COPYRIGHT 2002 ACS
TI Encyclopedia of explosives and related items. Volume 7. Hydrogen to lysol
SO U. S. NTIS, AD Rep. (1975), AD-A019502, 636 pp. Avail.: NTIS
From: Gov. Rep. Announce. Index (U. S.) 1976, 76(5), 200
CODEN: XADRCH

L12 ANSWER 3 OF 31 CAPLUS COPYRIGHT 2002 ACS
TI Disinfectants for use in tuberculosis institutions. I. Tuberculocidal effect of the Bulgarian disinfectants Veraform, Khlorin, Lysol, Manusterol B, and a combination of Perhydrol and liquid Sinpro
SO Epidemiol., Mikrobiol. Infek. Bolesti (1974), 11(1), 63-8
CODEN: EMIBA3

L12 ANSWER 4 OF 31 CAPLUS COPYRIGHT 2002 ACS
TI Fungistatic and fungicidal action of phenol, lysol, and formaldehyde on Coccidioides immitis 7/86, Histoplasma capsulatum 6652, and Blastomyces dermatitidis 6064
SO Zh. Mikrobiol., Epidemiol. Immunobiol. (1969), 46(1), 145-9
CODEN: ZMEIAV

L12 ANSWER 5 OF 31 CAPLUS COPYRIGHT 2002 ACS
TI A substitute for Lysol
SO Pharm. J. (1953), 170, 59-60

L12 ANSWER 6 OF 31 CAPLUS COPYRIGHT 2002 ACS
TI Gross amino-aciduria following a Lysol burn
SO Lancet (1952), 262, 190-2

L12 ANSWER 7 OF 31 CAPLUS COPYRIGHT 2002 ACS

TI Colorimetric evaluation of cresol in liquor cresolis saponatus or lysol
SO J. Proc. Inst. Chemists (India) (1950), 22, 58-64

L12 ANSWER 8 OF 31 CAPLUS COPYRIGHT 2002 ACS
TI Concentrations and time limits of Lysol dips. Report of the Research Committee, West Virginia Gladiolus Society
SO et al. Gladiolus Suppl. (1942), 6(No. 1), 10-12

L12 ANSWER 9 OF 31 CAPLUS COPYRIGHT 2002 ACS
TI Variation in the bactericidal value of Lysol, B. P.
SO Pharm. J. (1942), 148, 112

L12 ANSWER 10 OF 31 CAPLUS COPYRIGHT 2002 ACS
TI Preparation of lysol
SO Quart. J. Pharm. Pharmacol. (1938), 11, 538-42

L12 ANSWER 11 OF 31 CAPLUS COPYRIGHT 2002 ACS
TI Blood sugar, rest nitrogen and bilirubin in lysol poisoning
SO Wiener klin. Wochschr. (1932), 45, 1252-4

L12 ANSWER 12 OF 31 CAPLUS COPYRIGHT 2002 ACS
TI Corrosion of lysol containers
SO Chemist and Druggist (1932), 116, 6

L12 ANSWER 13 OF 31 CAPLUS COPYRIGHT 2002 ACS
TI Poisoning with apial, lysol, meta tablets, carbide, carbon monoxide and green oil
SO Nederland. Tijdschr. Geneeskunde (1931), 75, II, 2453-6

L12 ANSWER 14 OF 31 CAPLUS COPYRIGHT 2002 ACS
TI Pale cresylic acid and lysol
SO Quart. J. Pharm. Pharmacol. (1931), 4, 373-8

L12 ANSWER 15 OF 31 CAPLUS COPYRIGHT 2002 ACS
TI The condition of the blood from the qualitative point of view in carbon monoxide, lysol and aniline oil poisoning
SO Zentr. Gewerbehyg. Unfallverhüt. (1927), 14, 225-8
From: Chem. Zentr. 1927, II, 1732

L12 ANSWER 16 OF 31 CAPLUS COPYRIGHT 2002 ACS
TI Lysol
SO Pharm. J. (1926), 116, 409

L12 ANSWER 17 OF 31 CAPLUS COPYRIGHT 2002 ACS
TI Lysol
SO Pharm. Conference, Australasian Assoc. Adv. Sci. (1924) 7 pp.

L12 ANSWER 18 OF 31 CAPLUS COPYRIGHT 2002 ACS
TI Analysis of lysol
SO J. Soc. Chem. Ind. (1924), 43, 93-6

L12 ANSWER 19 OF 31 CAPLUS COPYRIGHT 2002 ACS
TI Approximate estimation of commercial cresol in lysol
SO Analyst (1921), 46, 451

L12 ANSWER 20 OF 31 CAPLUS COPYRIGHT 2002 ACS
TI The approximate estimation of commercial cresol in lysol
SO Pharm. J. (1921), 106, 479-80

L12 ANSWER 21 OF 31 CAPLUS COPYRIGHT 2002 ACS
TI Note on the detection of .beta.-naphthol in lysol and similar preparations
SO Analyst (1915), 40, 341-3

L12 ANSWER 22 OF 31 CAPLUS COPYRIGHT 2002 ACS
TI Cauterization of the Eye with Lysol and Potassium Permanganate
SO Klin. Monatsbl. Augenheilk. (1912), 12, 758; also in Zentr. Biochem.
Biophys., 12, 697-8

L12 ANSWER 23 OF 31 CAPLUS COPYRIGHT 2002 ACS
TI Quantitative Determination of Phenols in the Human Organs in a

Case of

Lysol Poisoning

SO Schweiz Wochschr. (1911), 49, 121-2

L12 ANSWER 24 OF 31 CAPLUS COPYRIGHT 2002 ACS
TI Comparative Tests of the Disinfecting Action of **Lysol**, Liquor
Cresoli Saponatus and Several Newer Disinfectants of Similar
Composition

SO Disinfection (1909), 1, 267

From: Chem. Zentr., 1909, 1, 206

L12 ANSWER 25 OF 31 CAPLUS COPYRIGHT 2002 ACS
TI **Lysol** and Carbol Tablets and the Applicability of the Raschig
Method to the Determination of m-Cresol in Cresol Tablets
SO Ber. pharm. Ges. (1909), 18, 421-30

L12 ANSWER 26 OF 31 CAPLUS COPYRIGHT 2002 ACS
TI Cresol Excretion in the Dog after **Lysol** Administration
SO Berlin. Therap. Monatsh. (1908), 22, 366-7

L12 ANSWER 27 OF 31 CAPLUS COPYRIGHT 2002 ACS
TI Toxicological Comparison between Chinosol, **Lysol**, and Cresol
SO Chem.-Ztg. (1908), 32, 23

L12 ANSWER 28 OF 31 CAPLUS COPYRIGHT 2002 ACS
TI Toxicological Comparison between Chinosol, **Lysol** and Cresol
SO Vierteljschr. ger. Med. [3] (1907), 34, 1-13

L12 ANSWER 29 OF 31 CAPLUS COPYRIGHT 2002 ACS
TI Urine Coloration after **Lysol** Poisoning
SO Beitr. Chem. Physiol. (Hofmeister) (1907), 10, 251-52

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TI Remarks and Explanations Relating to Wandel's Paper on the
Pathology of
Lysol and Cresol Poisoning
SO Arch. exp. Path. Pharm. (1907), 56, 416-19

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TI **Lysol** and Cresol Poisoning
SO Arch. Exp. Pathol. and Pharmacol. (1907), 56, 161-86

=> d ibib ab 16

L12 ANSWER 16 OF 31 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1926:20968 CAPLUS
DOCUMENT NUMBER: 20:20968
ORIGINAL REFERENCE NO.: 20:2563e
TITLE: **Lysol**
AUTHOR(S): Knight, W.
SOURCE: Pharm. J. (1926), 116, 409
DOCUMENT TYPE: Journal
LANGUAGE: Unavailable
AB To obviate the laborious Brit. Pharm. Codex method for making
lysol, put
into a 500 cc. bottle KOH 25.5 g. and H2O 30 cc.; when dissolved
add
industrial alc. 15 cc., linseed oil 113.6 g., shake and set aside for 1
day. To the soap thus completely formed, add glycerol 28.4 g., H2O
to
make 227.2 g., then add cresol 227.2 g., shake and allow to stand for
1
day. A clear, amber-colored liquid results.

=> s ld 50

11886 LD

2061 LDS

13651 LD

(LD OR LDS)

1599846 50

L13 264 LD 50

(LD(W)50)

=> s disinfect?

L14 73636 DISINFECT?

=> d his

(FILE 'HOME' ENTERED AT 16:02:22 ON 25 JUN 2002)

FILE 'MEDLINE' ENTERED AT 16:02:36 ON 25 JUN 2002

L1 50 S LYSOL

L2 0 S L1 NOT PY>88

L3 0 S L1 NOT PY>97

FILE 'CAPLUS' ENTERED AT 16:04:30 ON 25 JUN 2002

L4 286 S LYSOL

L5 3 S L4 NOT PY>97

L6 46435 S ANTISEPTIC

L7 98229 S KILL?

L8 1054 S L6 AND L7

L9 1 S L8 NOT PY>97

L10 984 S L8 NOT PY>1997

L11 280 S L4 NOT PY>1997

L12 31 S LYSOL/TI

L13 264 S LD 50

L14 73636 S DISINFECT?

=> log y

COST IN U.S. DOLLARS	SINCE FILE	TOTAL
	ENTRY	SESSION
FULL ESTIMATED COST		97.40 98.75

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)
SINCE FILE TOTAL

	ENTRY	SESSION
CA SUBSCRIBER PRICE		-0.62 -0.62

STN INTERNATIONAL LOGOFF AT 16:13:11 ON 25 JUN 2002